

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: September 14, 2003, 04:06:46 : Search time 64.5 Seconds

(without alignments)  
8646.160 Million cell updates/sec

Title: US-09-651-150B-1

Perfect score: 3490

Sequence: 1 aaagaggaagcagcgtgctc.....ttactctgtctcatccttt 1911

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 541936 seqs, 145912426 residues

Total number of hits satisfying chosen parameters: 1083872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
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-Q=/cgn2\_1/USPTO.spool/US09651150/runat\_12092003\_184345\_9763/app\_query.fasta\_1.2055  
-DB=published.Applications\_AA -OFFM=fastan -SUFFIX=rapb -MINMATCH=0.1  
-LOOPCL=0 -LOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsu62  
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZ=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US09651150.qcgn.1.1.74.#runat\_12092003\_184345\_9763  
-NCPU=6 -ICPU=3 -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pcp.\*
- 2: /cgn2\_1/USPTO.spool/US09651150/runat\_12092003\_184345\_9763/app\_query.fasta\_1.2055
- 3: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pcp.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pcp.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pcp.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pcp.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pcp.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pcp.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pcp.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pcp.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pcp.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pcp.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pcp.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pcp.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pcp.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pcp.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pcp.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description
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1	2047	58.7	390	10	US-09-135-238B-2	Sequence 2, Appli
2	741	21.2	255	11	US-09-866-050A-683	Sequence 683, App
3	331.5	9.5	84	10	US-09-135-238B-3	Sequence 3, Appli
4	233	6.7	43	10	US-09-135-238B-12	Sequence 12, Appli
5	200	5.7	608	10	US-09-950-294-4	Sequence 4, Appli
6	200	5.7	764	10	US-09-818-247-1	Sequence 1, Appli
7	200	5.7	764	10	US-09-981-353-59	Sequence 59, Appli
8	200	5.7	764	10	US-09-989-919-124	Sequence 124, App
9	200	5.7	764	12	US-09-949-039-65	Sequence 65, Appli
10	200	5.7	771	10	US-09-982-107-8	Sequence 8, Appli
11	200	5.7	771	12	US-09-949-039-68	Sequence 68, Appli
12	199	5.7	746	10	US-09-982-107-4	Sequence 4, Appli
13	197	5.6	771	10	US-09-818-247-4	Sequence 4, Appli
14	186	5.3	769	10	US-09-982-107-3	Sequence 3, Appli
15	186	5.3	769	10	US-09-982-107-10	Sequence 10, Appli
16	186	5.3	769	12	US-09-949-039-69	Sequence 69, Appli
17	185	5.3	602	14	US-10-047-542-51	Sequence 51, Appli
18	184	5.3	758	12	US-09-949-039-66	Sequence 66, Appli
19	183	5.2	732	10	US-09-818-247-5	Sequence 5, Appli
20	183	5.2	733	12	US-09-949-039-70	Sequence 70, Appli
21	182	5.2	757	10	US-09-818-247-2	Sequence 2, Appli
22	182	5.2	757	10	US-09-982-107-6	Sequence 6, Appli
23	182	5.2	757	12	US-09-949-039-67	Sequence 67, Appli
24	175.5	5.0	1734	10	US-09-862-027-81	Sequence 81, Appli
25	170.5	4.9	305	15	US-10-188-012-1	Sequence 1, Appli
26	168.5	4.8	772	12	US-09-949-039-71	Sequence 71, Appli
27	167.5	4.8	624	11	US-09-491-322-22	Sequence 22, Appli
28	167.5	4.8	624	12	US-10-372-614-22	Sequence 22, Appli
29	167.5	4.8	771	12	US-09-969-748C-13	Sequence 13, Appli
30	167.5	4.8	771	12	US-09-949-039-99	Sequence 99, Appli
31	167.5	4.8	773	10	US-09-818-247-6	Sequence 6, Appli
32	167.5	4.8	773	10	US-09-982-107-2	Sequence 2, Appli
33	167	4.8	903	15	US-10-156-761-11093	Sequence 11093, A
34	166.5	4.8	917	12	US-10-017-161-1598	Sequence 1598, Ap
35	165.5	4.7	1386	12	US-10-327-414-2	Sequence 2, Appli
36	158	4.5	1298	10	US-09-825-288A-2	Sequence 2, Appli
37	157.5	4.5	1115	15	US-10-322-579-17	Sequence 17, Appli
38	157.5	4.5	1479	15	US-10-156-761-11739	Sequence 11739, A
39	156.5	4.5	797	15	US-10-156-761-10907	Sequence 10907, A
40	155	4.4	881	9	US-09-816-860A-2	Sequence 2, Appli
41	154	4.4	375	15	US-10-156-761-14622	Sequence 14622, A
42	153.5	4.4	3122	12	US-10-200-562-201	Sequence 201, App
43	153.5	4.4	3122	12	US-10-237-551-201	Sequence 250, App
44	153.5	4.4	3122	12	US-10-237-551-250	Sequence 161, App
45	153	4.4	825	12	US-10-200-562-161	

ALIGNMENTS

RESULT 1  
US-09-135-238B-2  
: Sequence 2, Application US/09135238B  
: Patent No. US20020177565A1  
: GENERAL INFORMATION:  
: APPLICANT: No. US20020177565Alan, Garry P.  
: APPLICANT: Hitoshi, Yasumichi  
: TITLE OF INVENTION: TOSO  
: FILE REFERENCE: A65635-1/DJB/RMS  
: CURRENT APPLICATION NUMBER: US/09/135,238B  
: PRIOR FILING DATE: 1998-08-17  
: PRIOR APPLICATION NUMBER: 60/066,063  
: PRIOR FILING DATE: 1997-11-17  
: NUMBER OF SEQ ID NOS: 31  
: SOFTWARE: PatentIn Ver. 2.0  
: SEQ ID NO 2  
: LENGTH: 390  
: TYPE: PRI  
: ORGANISM: Homo sapiens  
US-09-135-238B-2

Alignment Scores:	8.09e-133	Length:	390
Pred. No.:	2047.00	Matches:	389

Percent Similarity:	99.74%	Conservative:	0
Best Local Similarity:	99.74%	Mismatches:	1
Query Match:	58.65%	Indels:	0
DB:	10	Gaps:	0
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Qy	74	ATGACATCTGGCTTGGCCACTTTACTTCTGCGCATATCAGGGGCCCTGAGATCCTC	133
Db	1	MetAspArgTrpLeuTrpProLeuTyrPheLeuProValSerGlyAlaLeuArgIleLeu	20
Qy	134	CCAGAACTAAAGTAGAGGGAGCTGGCGGATCAGTTACCATCAATGCCACATTCCT	193
Db	21	ProGluValLysValGluGlyLeuGlyCysValThrIleLysCysProLeuPro	40
Qy	194	GAATGCATGTAGGATATATCTGTGCGCGGAGATGGCTGGAACATGTGGTACC	253
Db	41	GluMetHisValArgMetTyrPheLeuValLysValThrIleLysCysProLeuPro	40
Qy	314	TACCCACGCAAGATCTGTTCTAGTGGAGGTATACACAGCTGACAGAAAGTGCACAGCGGA	373
Db	80	CysLeuAspLysLysLeuPheLeuValGluMetThrGlnLeuThrGluAsnAspGly	99
Qy	374	GTCTATGCTCGCTGGAGCGGCATGAACACACACCGGGGAAAGACCCAGAAAGTCAACCTG	433
Db	100	IleTyrAlaCysGlyValGlyMetLysThrAspLysThrGlyLysThrGlnLysIleThrLeu	119
Qy	434	AATGTCCACAGTGAATAC---GAGCCATCATGTGGGAAGACGACCAATGCCTGAGACTCCA	490
US-09-651-150B-1 (1-1911) x US-09-866-050A-683 (1-255)			
Qy	74	ATGACATCTGGCTTGGCCACTTTACTTCTGCGCATATCAGGGGCCCTGAGATCCTC	133
Db	1	MetAspPheTrpLeuTrpLeuLeuTyrPheLeuProValSerGlyAlaLeuArgValLeu	20
Qy	134	CCAGAACTAAAGTAGAGGGAGCTGGCGGATCAGTTACCATCAATGCCACATTCCT	193
Db	21	ProGluValGlnLeuAsnValGluTrpGlySerIleLeuLeuGluCysProLeuPro	40
Qy	194	GAATGCATGTAGGATATATCTGTGCGCGGAGATGGCTGGAACATGTGGTACC	253
Db	41	GlnLeuHisValArgMetTyrLeuCysArgGlnMetAlaLysProGlyLysCysThr	60
Qy	254	GTGTATCTCCACCAACTTCATCAAGCGACAATACAAGGCCGAGTTACTCTGAAGCAA	313
Db	61	ValValSerAsnThr---PheValLysLysGluTyrGluArgArgValThrLeuThrPro	79
Qy	314	TACCCACGCAAGATCTGTTCTAGTGGAGGTATACACAGCTGACAGAAAGTGCACAGCGGA	373
Db	80	CysLeuAspLysLysLeuPheLeuValGluMetThrGlnLeuThrGluAsnAspGly	99
Qy	374	GTCTATGCTCGCTGGAGCGGCATGAACACACACCGGGGAAAGACCCAGAAAGTCAACCTG	433
Db	100	IleTyrAlaCysGlyValGlyMetLysThrAspLysThrGlyLysThrGlnLysIleThrLeu	119
Qy	434	AATGTCCACAGTGAATAC---GAGCCATCATGTGGGAAGACGACCAATGCCTGAGACTCCA	490
Alignment Scores:			
Pred. No.:	6,11e-43	Length:	255
Score:	741.00	Matches:	145
Percent Similarity:	59.65%	Conservative:	34
Best Local Similarity:	56.42%	Mismatches:	70
Query Match:	21.23%	Indels:	8
DB:	11	Gaps:	4
US-09-651-150B-1 (1-1911) x US-09-866-050A-683 (1-255)			
APPLICANT: Watson, James D.			
APPLICANT: Strachan, Lorna			
APPLICANT: Sleeman, Matthew			
APPLICANT: Onrust, Rene			
APPLICANT: Murison, James G.			
TITLE OF INVENTION: Compositions Isolated From Skin Cells			
TITLE OF INVENTION: and Methods for Their Use			
FILE REFERENCE: 11000.1011C4U			
CURRENT APPLICATION NUMBER: US/09/866,050A			
CURRENT FILING DATE: 2001-05-24			
NUMBER OF SEQ ID NOS: 725			
SOFTWARE: FastSeq for Windows Version 4.0			
SEQ ID NO 683			
LENGTH: 255			
TYPE: PRT			
ORGANISM: Mouse			
US-09-866-050A-683			

Db 120 AsnValHisAsnGluTyrProGluProPheTyrGluAspGluTyrThrSerGluArgPro 139  
QY 491 AAATGGTTTCATCTGCCCTTAITGTTCCAGATGCCT-----GCATATGCC 535  
Db 140 ArgTyrLeuHisArgPheLeuGlnHisGlnMetProTyrPheLeuHisGlySerGluHisPro 159  
QY 536 AGTTCTTCCAAATTCGTAACAGAGTTTACCACACAGCTCAAGAGGGGCAAGGTCCCTCCA 595  
Db 160 SerSerSerGlyValIleAlaIleValThrProAlaSerTyrThrGluAlaProPro 179  
QY 596 GTTCACACATCTCTCCGCCACACACCAATCAACCCAGCCCTCGAGTGTCCAGAGCATCT 655  
Db 180 ValHisGlnProSerSerIleThrSerValThrGlnHisProArgValTyrArgAlaPhe 199  
QY 656 TCAGTAGCAGGTGACAGCCCGGACCACTTCTGCCATCCACTCAGCTCAAAAATCTCA 715  
Db 200 SerValSerAlaThrTyrSerProAlaLeuLeuProAlaThrThrAlaSerLysThrSer 219  
QY 716 GCTCTGGAGGGGTGCTCAAGCCCGCAGACGCCAGCTACACACACACAGGCTGCAC 775  
Db 220 ThrGlnGlnAla---IleArgProLeuGluAlaSerTyrSerHisHisThrArgLeuHis 238  
QY 776 AGCAGAGACACTGGACTATGCTACACTCTGGGAGGGAAGGCCAAGGA 826  
Db 239 GluGlnArgThrArgHisHisGlyProHisTyrGlyArgGluAspArgGly 255

RESULT 3  
US-09-135-238B-3  
; Sequence 3, Application US/09135238B  
; Patent No. US20020177565A1  
; GENERAL INFORMATION:  
; APPLICANT: No. US20020177565Alan, Garry P.  
; APPLICANT: Hitoshi, Yasumichi  
; TITLE OF INVENTION: TOSO  
; FILE REFERENCE: A65635-1/DJB/RMS  
; CURRENT APPLICATION NUMBER: US/09/135,238B  
; CURRENT FILING DATE: 1998-08-17  
; PRIOR APPLICATION NUMBER: 60/066,063  
; PRIOR FILING DATE: 1997-11-17  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 84  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (13)..(16)  
; OTHER INFORMATION: The xaa at positions 13 through 16 represents an  
; OTHER INFORMATION: unknown amino acid.  
; NAME/KEY: UNSURE  
; LOCATION: (44)..(48)  
; OTHER INFORMATION: The xaa at positions 44 through 48 represents an  
; OTHER INFORMATION: unknown amino acid.  
; NAME/KEY: UNSURE  
; LOCATION: (61)..(62)  
; OTHER INFORMATION: The xaa at positions 61 and 62 represents an  
; OTHER INFORMATION: unknown amino acid.  
US-09-135-238B-3

Alignment Scores:  
Pred. No.: 8,01e-15 Length: 84  
Score: 331.50 Matches: 69  
Percent Similarity: 84.52% Conservative: 2  
Best Local Similarity: 82.14% Mismatches: 2  
Query Match: 9.50% Indels: 11  
DB: 10 Gaps: 3  
US-09-651-150b-1 (1-1911) x US-09-135-238B-3 (1-84)  
QY 170 GTTACATCAATGCCACTTCTGAAATGCATGTG-----AGGATATATCTG 217  
|||||

Db 1 ValThrIleLysCysProLeuProGluMetHisVal\*\*\*\*\*ArgIleTyrLys 20  
QY 218 TGCCGGGAGATGGGTGATCTGGAACATGTGGTACCGTGTATCCACACCAACTTCATC 277  
Db 21 CysArgGluAsnAlaGlySerGlyThrCysGlyThrValValSerThrThr\*\*\*PheIle 40  
QY 278 AAGCGCAAA-----TACAAGGCGCGAGTTACTCTGAAGCAATACCCAGGC 322  
Db 41 LysAlaGlu\*\*\*\*\*TyrIlyGlyArgValThrLeuLysGlnTyrProArg 60  
QY 323 -----AAGATCTCTTCTAGTAGGAGTAACACAGCTGACAGAAAGTGACAGCGAGTC 376  
Db 61 \*\*\*\*\*LysAsnLeuPheLeuValGluValThr\*\*\*LeuThrGluSerAspSerGlyVal 80  
QY 377 TATCCCTGCGGA 388  
Db 81 TyrAlaCysGly 84

RESULT 4  
US-09-135-238B-12  
; Sequence 12, Application US/09135238B  
; Patent No. US20020177565A1  
; GENERAL INFORMATION:  
; APPLICANT: No. US20020177565Alan, Garry P.  
; APPLICANT: Hitoshi, Yasumichi  
; TITLE OF INVENTION: TOSO  
; FILE REFERENCE: A65635-1/DJB/RMS  
; CURRENT APPLICATION NUMBER: US/09/135,238B  
; CURRENT FILING DATE: 1998-08-17  
; PRIOR APPLICATION NUMBER: 60/066,063  
; PRIOR FILING DATE: 1997-11-17  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 43  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-135-238B-12  
Alignment Scores:  
Pred. No.: 4,37e-08 Length: 43  
Score: 233.00 Matches: 43  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 6.68% Indels: 0  
DB: 10 Gaps: 0  
US-09-651-150B-1 (1-1911) x US-09-135-238B-12 (1-43)

QY 971 CAGAGGCGCGGGTGGCGCGCGCGCTCCCAAAACAACATCTACAGCGCTGCCG 1030  
Db 1 GluArgProArgGlySerProArgProArgProArgSerGlnAsnIleTyrSerAlaCysPro 20  
QY 1031 CGCGCGCTCGTGGAGCGGACGCTGACAGGACAGGAGGAGGCGCGCTCCGCGCGCGGA 1090  
Db 21 ArgArgAlaArgGlyAlaAspAlaAlaGlyThrGlyGluAlaProValProGlyProGly 40  
QY 1091 GCGCGCTGTG 1099  
Db 41 AlaProLeu 43

RESULT 5  
US-09-950-294-4  
; Sequence 4, Application US/09950294  
; Patent No. US20020127645A1  
; GENERAL INFORMATION:  
; APPLICANT: Morrison, Sherie L.  
; Chintalacharuvu, Kote R.  
; TITLE OF INVENTION: SECRETORY IMMUNOGLOBULIN PRODUCED  
; BY SINGLE CELLS AND METHODS FOR MAKING AND USING  
; SAME  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt  
 STREET: 11150 Santa Monica Boulevard, Suite 400  
 CITY: Los Angeles  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 90025

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq for Windows Version 2.0

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/950,294

FILING DATE: 10-Sep-2001

CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/095,385

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Canady, Karen S

REGISTRATION NUMBER: 39,927

REFERENCE/DOCKET NUMBER: 30435.45USU1

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 310 445-1140

TELEFAX: 310 445-9031

TELEX: <Unknown>

## INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 608 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-950-294-4

## Alignment Scores:

Pred. No.:	1,22e-05	Length:	608
Score:	200.00	Matches:	115
Percent Similarity:	35.11%	Conservative:	76
Best Local Similarity:	21.14%	Mismatches:	186
Query Match:	5.73%	Indels:	167
DB:	10	Gaps:	20

US-09-651-150B-1 (1-1911) x US-09-950-294-4 (1-608)

Qy	79	CTTCTGGCTTGGCCACTTACTTCCCTCCAGTATCAGGGGGCCCTGAGGATCCTCCACAGA	138
Db	6	LeuThrCysLeuLeuAlaValPheProAla-IleSerThrLysSerProIlePheGlyPr	25
Qy	139	AGTAAAGGTAGAGGGGAGTGGCGGATCAGTACCATCAATGCCACTTCTCT	193
Db	25	oGluGluValAsnSerValGluGlyAsnSerValSerIleThrCysTyrTyrProTh	45
Qy	194	-----GAATCATGTGAGGATATATCTGCGCGGAGATGGCTGATGATGGAACATG	246
Db	45	rSerValAsnArgHisThrArgLysTyrTyrPcysArgGlnGlyAlaArgGlyGly---Cy	64
Qy	247	TGTTACCGTGGTATCCACCACTTCATCAAGCAGCAATACAGGCGCCAGTTACTCT	306
Db	64	sIleThrLeuIleSerSerGluGlyTyrValSerSerLysTyrAlaGlyArgAlaAsnLe	84
Qy	307	GAGCAATACCCAGCGAAGATCTGTCCTAGTGGAGGTACACAGTGCAGAAAGTGA	366
Db	84	uThrAsnPheProGluAsnGlyThrPheValValAsnIleAlaGlnLeuSerGlnAspAs	104
Qy	367	CAGCGAGTCTATGCTCGCGGAGCGGCATGAACACA	403
Db	104	pSerGlyArgTyrLysCysGlyLeuGlyIleAsnSerArgGlyLeuSerPheAspValSe	124
Qy	404	-----GACCG	408
Db	124	rLeuGluValSerGlnGlyProGlyLeuLeuAsnAspThrLysValTyrThrValAspLe	144

Qy	409	GGGAAGACCCAGAAAGTCCACCTGAATGTCCACAGTGAATACAGAGCCATCAGGGGAAGA	468
Db	144	uGlyArgThr-----ValThrIleAsnCysProPheLysThrGluAsnAlaGlnLysAr	162
Qy	469	GCAGCCAATGCCTGAGACTCCAAAATGGTTTCATCTGCCCTATTTGTTCCAGATGCCCTGC	528
Db	162	gLysSerLeuTyrIlys-----GlnIleGlyLe	171
Qy	529	ATATGCCAGTTCTT-----CCAAATTCGTAAACACAGT	561
Db	171	uTyr-ProValLeuValIleAspSerSerGlyTyrValAsnProAsnTyrThrGlyArgI	191
Qy	562	TACCACACAGCTCAAAAGGGCAAGTCCCTCCAGTTCACACATCCCTCCGCCACACCCA	621
Db	191	leArgLeuAspIleGlnGlyThrGlyGlnLeuPheSerValIleAsnGlnLeuA	211
Qy	622	AATCACCACCGCCCTCGAG-----TGT-----CCAG	648
Db	211	rgLeuSerAspAlaGlyGlnTyrLeuCysGlnAlaGlyAspAspSerAsnSerAsnLysL	231
Qy	649	AGCATCTTCAGTAGCAGGTGACAAAGCCGCAACCTCTGCTGCATCCACTACAGCTCAAA	708
Db	231	ysAsnAlaAspLeuGlnValLeuLysProGlu-LeuValTyrGluAspLeuArg	250
Qy	709	AATCTCAGCTCTGGAGGGCTGTCAAGCCGCCAGACGCC-----	747
Db	251	GlySerValThrPheHisCysAlaLeuGlyProGluValAlaAsnValAlaLysPheLeu	270
Qy	748	-----CAGCTACAAACACACACAGGCTCCACAGGAGAGACACTGGACTATGGCTC	801
Db	271	CysArgGlnSerSerGlyGluAsnCysAspValValValAsnThrLeuGlyLysArgAla	290
Qy	802	ACAGTCTGGAGGAGGCAAGGATTTCACATCTCCATCCCGACCATCTGGGCTTT	861
Db	291	ProAlaPheGluGlyArgIleLeuLeuAsnProGlnAspLysAsp-----GlySerPhe	308
Qy	862	CCTGCTGGCACTTCTGGGCTGGTGTAA-----	891
Db	309	SerValValIleThrGlyLeuArgLysGluAspAlaGlyArgTyrLeuCysGlyAlaHis	328
Qy	892	---AAGGGCGTTCAAAGGAGAAAGCCCTCTCCAGGCGGCGCCCGACCTGGCGGTGAG	948
Db	329	SerAspGlyGlnLeuGlnGlySerProIleGlnAlaTrpGlnLeuPheValAsnGlu	348
Qy	949	GATCGCGCCCTGGAGAGTCCACAGAGCCCGCGGGTCCGCGACCGCGCTCCCAAAA	1008
Db	349	GlusSer-----ThrIleProArgSerProThrValVal-LysGlyValAlaGlySe	365
Qy	1009	CAACATCTACAGCCCTCCCGCGCGCTCTGGAGCG-----	1048
Db	365	rSerValAlaValLeuCysProTyrAsnArgLysGlnSerLysSerIleLysTyrTrpCy	385
Qy	1049	-----GACGCTGCAGGCACAGGGGCGCGCTCCCGCTCCCGCGCGCGCGCTTGC	1101
Db	385	sLeuTrpGluGlyAlaGlnAsnGlyArg-----	394
Qy	1102	CCCGCGCGCGCTGAGGGTCTGATCTCCCTGGCTCCATCCCGCTCTGGAACACAG	1161
Db	395	---CysProLeuLeuValAspSerGluGlyTrpValIysAla-----	407
Qy	1162	CTGTGAATAC-----GTGAGCTCTACACACAGCTGCC-----	1195
Db	408	---GlnTyrTyrGluGlyArgLeuSerLeuGluGluProGlyAsnGlyThrPheThrVa	426
Qy	1195	-----	1195
Db	426	IleLeuAsnGlnLeuThrSerArgAspAlaGlyPheTyrTrpCysLeuThrAsnGlyAs	446
Qy	1196	-GCCATGATGAGACAGTATTCAGATCATCATCAATGTCCTGCTGCTGACACTCCC	1254
Db	446	pThrLeu-TrpArgThrThrValGluIleLys-----IleIleGluGlyGluP	462

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QY 1255 CAGCTATATCCCAACCCAGCGCTGGGACTGTGTGCAAGAGTCTCATCTATCTGCTGA 1314
    || :::: ||| ||| |||
Db 462 rAsnLeuLysValProGlyAsnValThrAlaVal-----L 474

QY 1315 TGTCCAAATCATCTTCATGTCGTCAGAGCGCTCATCACTTCCCATGCCCAICTCGA 1374
    :: :::: ||| ||| ||| ||| ||| |||
Db 474 ecglyGluThrLeu-----LysValProCysHisPheProCysLysPheSerS 490

QY 1375 CT 1376
    ::
Db 490 er 490

RESULT 6
US-09-818-247-1
; Sequence 1, Application US/09818247
; Patent No. US20020102657A1
; GENERAL INFORMATION:
; APPLICANT: Mostov, Keith E.
; APPLICANT: Chapin, Steven J.
; APPLICANT: Richman-Eisenstat, Janice
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Ligands Directed to the No. US20020102657A1-Secretory Component.
; TITLE OF INVENTION: No US20020102657A1-Stalk Region of p1gR and Methods of Use Therein
; FILE REFERENCE: 18062E-0009100S
; CURRENT APPLICATION NUMBER: US/09/818,247
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: WO PCT/US01/09699
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/192,197
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,198
; PRIOR FILING DATE: 2000-03-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 764
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human polymeric Immunoglobulin receptor (p1gR)
US-09-818-247-1

Alignment Scores:
Pred. No.: 1.26e-05 Length: 764
Score: 200.00 Matches: 115
Percent Similarity: 35.11% Conservative: 76
Best Local Similarity: 21.14% Mismatches: 186
Query Match: 5.73% Indels: 167
DB: 10 Gaps: 20

US-09-651-150B-1 (1-1911) x US-09-818-247-1 (1-764)
QY 79 CTTCGTGCTTTGCCACTTTTCTTCCTGCCAGTATCAGGGGGCCTGAGGATCCTCCAGA 138
    ||| ||| :::: ||| ||| ||| ||| |||
Db 6 LeuThrCysLeuLeuAlaValPheProAla-IleSerThrLysSerProIlePheGlyPr 25
    :::: ||| ||| ||| ||| ||| ||| ||| |||
QY 139 AGTAACGTAGAGGGGGAGCTGGCGGATCAGTTTACCATTCAATCAATGCCACTTCTCT 193
    :::: ||| ||| ||| ||| ||| ||| ||| |||
Db 25 oGluGluValAsnSerValGluGlyAsnSerValSerIleThrCysTyrTyrProProth 45
    :::: -GAAATGCATCTGAGGATATATCTGTCCGGGAGATGCTGGATCTCGAACATG 246
    ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 194 -----GAAATGCATCTGAGGATATATCTGTCCGGGAGATGCTGGATCTCGAACATG 246
    ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 45 rSerValAsnArgHisThrArgLysTyrTyrCysArgGluGlyAlaArgGlyGly---Cy 64
    ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 247 TGGTACCGTGGTATCCACCACCACTTCATCAGGCAGATACAGGGCGCGAGTTACTCT 306
    | ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 64 sIleThrLeuIleSerSerGluGlyTyrValSerSerLysTyrAlaGlyArgAlaAsnLe 84
    ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 307 GAACCAATACCCAGCAGAATCTGTTCTTAGTGAGGTAAACACGCTGACAGAAAGTGA 366
    ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 84 uThrAsnPheProGluAsnGlyThrPheValValAsnIleAlaGlnLeuSerGlnAspAs 104
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QY 367 CAGCGGAGTCTATCCCTCGGAGCGGCGATGAACACA----- 403

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QY 1196 -GCCATGATGAGGACAGTGTGATGAGTACTACATCAATGTTCTGCTGACAACTCCC 1254  
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 446 pThrLeu-TrpArgThrThrValGluIleLys-----IleIleGluGlyGluP 462  
 QY 1255 CAGCTATCCCAACCCAGCTGGAGTGGTGGCCAAAGGAGTCTCATCTATCTGCTGA 1314  
 Db || : : : : :  
 462 roAsnLeuLysValProGlyAsnValThrAlaVal-----L 474  
 QY 1315 TGTCCATACCTGCTTCAATGTTCTCAGAGCCCTCATCTCCATGCCCCCACTCGA 1374  
 Db : ||||| : : : : :  
 474 euGlyGluThrLeu-----LysValProCysHisPheProCysLysPheSerS 490  
 QY 1375 CT 1376  
 Db : :  
 490 er 490

RESULT 9  
 US-09-949-039-65  
 ; Sequence 65, Application US/09949039  
 ; Publication No. US20030166160A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HAWLEY, STEPHEN B.  
 ; TITLE OF INVENTION: COMPOUNDS AND MOLECULAR COMPLEXES COMPRISING MULTIPLE  
 ; TITLE OF INVENTION: BINDING REGIONS DIRECTED TO TRANSCYTOTIC LIGANDS  
 ; FILE REFERENCE: 057220/1301  
 ; CURRENT APPLICATION NUMBER: US/09/949,039  
 ; CURRENT FILING DATE: 2001-09-06  
 ; NUMBER OF SEQ ID NOS: 114  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 65  
 ; LENGTH: 764  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-949-039-65

Alignment Scores:  
 Pred. No.: 1.26e-05 Length: 764  
 Score: 200.00 Matches: 115  
 Percent Similarity: 35.11% Conservative: 76  
 Best Local Similarity: 21.14% Mismatches: 186  
 Query Match: 5.73% Indels: 167  
 DB: 12 Gaps: 20

US-09-651-150B-1 (1-1911) x US-09-949-039-65 (1-764)

QY 79 CTCTGGCTTTGGCCACTTACTTCCTCCAGTATCAGGGGCCCTGAGATCCTCCACA 138  
 Db ||||| : : : : :  
 6 LeuThrCysLeuLeuAlaValPheProAla-IleSerThrLysSerProIlePheGlyPr 25  
 QY 139 AGTAAAGTAGAGGGGAGCTGGCGGATCAGTACATCAATCAATGCCACTTCCT- 193  
 Db : ||||| : : : : :  
 25 oGluGluValAsnSerValGluGlyAsnSerValSerIleThrCysTyrTyrProTh 45  
 QY 194 -----GAAATGCATGTGAGATATATCTGTGCGGCGAGATGCTGGATCGAACATG 246  
 Db ||||| : : : : :  
 45 rSerValAsnArgHisThrArgLysTyrTrpCysArgGlnGlyAlaArgGlyGly--Cy 64  
 QY 247 TGGTACCGTGGTATCCACCACCAACTTCATCAAGCGCAGATACAGGGCCGAGTACTCT 306  
 Db ||||| : : : : :  
 64 sIleThrLeuIleSerSerGluGlyTyrValSerSerLysTyrAlaGlyArgAlaAsnLe 84  
 QY 307 GAACCAATACCCAGCAGAAATCTGTTCCTAGTGGAGGTAAACAGCTGACAGAAAGTGA 366  
 Db ||||| : : : : :  
 84 uThrAsnPheProGluAsnGlyThrPheValValAsnIleAlaGlnLeuSerGlnAspAs 104  
 QY 367 CAGCGGAGTCTATCCCTGGGAGCGGCATGAACACA----- 403  
 Db ||||| : : : : :  
 104 pSerGlyArgTyrLysCysGlyLeuGlyIleAsnSerArgGlyLeuSerPheAspValSe 124  
 QY 404 -----GACCG 408  
 Db : : : : :  
 124 rLeuGluValSerGlnGlyProGlyLeuLeuAsnAspThrLysValTyrThrValAspLe 144

QY 409 GGGAAAGACCCAGAAAGTCACCTGAATGTCCACAGTGAATACGAGCCATCATGGAGA 468  
 Db ||||| : : : : :  
 144 uGlyArgThr-----ValThrIleAsnCysProPheLysThrGluAsnAlaGlnLysAr 162  
 QY 469 GCAGCAATCGCTGAGACTCCAAAATGGTTTCATCGCCCTATTGTTCAGATGCTGCG 528  
 Db : : : : :  
 162 glysSerLeuTyrLys-----GlnIleGlyLe 171  
 QY 529 ATATCCAGTCTCTT-----CCAAATTCGTAAACCAGACT 561  
 Db ||||| : : : : :  
 171 uTyr-ProValLeuValIleAspSerSerGlyTyrValAsnProAsnTyrThrGlyArgI 191  
 QY 562 TACACACAGCTCAAGGGCAAGTCCCTCAGTTCACCATCCCTCCCTCCACCACCCACA 621  
 Db : : : : :  
 191 leArgLeuAspIleGlnGlyThrGlyGlnLeuLeuPheSerValIleAsnGlnLeuA 211  
 QY 622 AATCACCACCCCTCGAG-----TGT-----CCAG 648  
 Db : : : : :  
 211 rgLeuSerAspAlaGlyGlnTyrLeuCysGlnAlaGlyAspSerAsnSerAsnLysL 231  
 QY 649 AGCATCTTCAGTAGCAGGTGACAGCCCGCAACCTTCCTGCCATCCACTACAGCTCAAA 708  
 Db : : : : :  
 231 ysAsnAlaAspLeuGlnValLeuLysProGluProGlu-LeuValTyrGluAspLeuArg 250  
 QY 709 AATCTCAGCTCTGGAGGGCTGCTCAAGCCCGCAGAGCC----- 747  
 Db : : : : :  
 251 GlySerValThrPheHisCysAlaLeuGlyProGluValAlaAsnValAlaLysPheLeu 270  
 QY 748 -----CAGCTACACACCACACAGGCTGCACAGGAGAGAGACAGCTGAGTATGGTTC 801  
 Db ||||| : : : : :  
 271 CysArgGlnSerSerGlyGluAsnCysAspValValValAsnThrLeuGlyLysArgAla 290  
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 Db : : : : :  
 291 ProAlaPheGluGlyArgIleLeuLeuAsnProGlnAspLysAsp-----GlySerPhe 308  
 QY 862 CTGCTGCCTCTCTGGGCTGTGGTGAA----- 891  
 Db : : : : :  
 309 SerValValIleThrGlyLeuArgLysGluAspAlaGlyArgTyrLeuCysGlyAlaHis 328  
 QY 892 ---AAGGCCGTTGAAAGGAGGAAAGCCCTCTCCAGGCGGGCCGCCAGCTGCCGTGAG 948  
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 329 SerAspGlyGlnLeuGlnGlySerProIleGlnAlaTrpGlnLeuPheValAsnGlu 348  
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 349 GluSer-----ThrIleProArgSerProThrValVal-LysGlyValAlaGlySe 365  
 QY 1009 CAACATCTACAGCGCTGCCCGCGCGCGCTGCTGGAGCG----- 1048  
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 365 rSerValAlaValLeuCysProTyrAsnArgLysGluSerLysSerIleLysTyrTrpCy 385  
 QY 1049 -----GACGCTGCAGGCAGGAGGCGCCCGCTTCCCGCGCGCGCGCGCTGCC 1101  
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 385 sLeuTrpGluGlyAlaGlnAsnGlyArg----- 394  
 QY 1102 CCGCGCGCGCTGAGGTGTCTGAATCTCCCTGGCTCCATGCCCATCTCTGAAGACCAG 1161  
 Db ||||| : : : : :  
 395 ---CysProLeuValAspSerGluGlyTrpValLysAla----- 407  
 QY 1162 GTGTGATATAC-----GTGAGCTCTACACACAGCTGCC----- 1195  
 Db : : : : :  
 408 ---GlnTyrGluGlyArgLeuSerLeuGluGluProGlyAsnGlyThrPheThrVa 426  
 QY 1195 ----- 1195  
 Db : : : : :  
 426 lIleLeuAsnGlnLeuThrSerArgAspAlaGlyPheTyrTrpCysLeuThrAsnGlyAs 446  
 QY 1196 -GCCATGATGAGGACAGTGTATCAGTACTACATCAATGTTCTGCTGACAACTCCC 1254  
 Db : : : : :  
 446 pThrLeu-TrpArgThrThrValGluIleLys-----IleIleGluGlyGluP 462







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; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Ligands Directed to the No. US20020102657A1-Secretory Component,
; TITLE OF INVENTION: No. US20020102657A1-Stalk Region of pIgR and Methods of Use Thereof
; FILE REFERENCE: 18062E-0009100S

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; FILE REFERENCE: EPI3002E
; CURRENT APPLICATION NUMBER: US/09/982.107
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 769
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-982-107-10

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US-09-651-150B-1 (1-1911) x US-09-982-107-10 (1-769)

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4 SerLeuPheAlaLeuLeuValThrValPheSer-----GlyVal 16

QY 91 CCCACTTTACTTCCTGCCAGTATCAGGGGCCCTGAGGATCCTCCAGAAAGTAAGGTAGA 150
Db  ::::| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
17 SerThrGlnSerPro-----IlePheGlyProGlnAsp-ValSerSerIleGlu----- 32

QY 151 GGGGAGCTGGCGGATCAGTTACCATCAATGCCACTTCTGTGAA-----AT 198
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33 -----GlyAsnSerValSerIleThrCysTyrTyrProAspThrSerValAsnAr 49

QY 199 GCATGTGAGGATATATCTGCCGGAGATGGCTGGATCTGGACATGTGTTACCGTGGT 258
Db  ||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
49 gHisThrArgLysTyrTrpCysArgGlnGlyAla---AsnGlyTyrCysAlaThrLeuIl 68

QY 259 ATCCACCACCAACTTCATCAGGCAGATACAGGGCCGAGTTACTCTGAAGCAATACCC 318
Db  ::::| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
68 eSerSerAsnGlyTyrLeuSerLysGluTyrSerGlyArgAlaSerLeuIleAsnPhePr 88

QY 319 ACACAAGAAATCTGTCTAGTGGAGGTAACACAGCTGACAGAAAAGTACAGCGAGTCTA 378
Db  | ::::| | | | | | | | | | | | | | | | | | | | | | | | | | | |
88 oGluAsnSerThrPheValIleAsnIleAlaHisLeuThrGlnGluAspThrGlySerTy 108

QY 379 TGCCTGGCGGCGGCATGACACAGACCGGGGAAAGACCCAGAAAGTCACCCCTGAATGT 438
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108 rLysCysglyLeugly---ThrThrAsnArgglyLeuPheAspValSerLeuGluVa 127

QY 439 CCACAGTGAATACGAGCCATCATGGGAAGACGAGCAATGCTGAGACTCCGAAATGGTT 498
Db  |-----SerGlnValProGluPheProAsnAspTh 137

QY 499 TCATCTG 505
Db  |||||
137 rHisVal 139
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Search completed: September 14, 2003, 04:22:31  
Job time : 91.5 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: September 14, 2003, 02:14:10 ; Search time 24 Seconds

(without alignments)  
6738.004 Million cell updates/sec

Title: US-09-651-150B-1

Perfect score: 3490

Sequence: 1 aaagagtaagcagcgtgc.....ttactctgtccatcccttt 1911

Scoring table:

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 657434

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- Issued Patents AA:\*  
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3: /cgn2.6/ptodata/2/iaa/6A.COMB.pcp:\*  
4: /cgn2.6/ptodata/2/iaa/6B.COMB.pcp:\*  
5: /cgn2.6/ptodata/2/iaa/PCTUS.COMB.pcp:\*  
6: /cgn2.6/ptodata/2/iaa/backfiles1.pcp:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2056	58.9	390	3	US-08-961-564A-2
2	2047	58.7	390	4	US-09-050-861B-2
3	1194.5	34.2	422	4	US-09-724-864-45
4	559	16.0	107	3	US-08-961-564A-4
5	380	10.9	73	4	US-09-050-861B-3
6	233	6.7	43	4	US-09-050-861B-12
7	200	5.7	608	4	US-09-095-385-4
8	200	5.7	771	3	US-08-434-000A-8
9	200	5.7	771	4	US-09-312-157-8
10	199	5.7	746	3	US-08-434-000A-4
11	199	5.7	746	4	US-09-312-157-4
12	187	5.4	109	3	US-08-961-564A-9

13	186	5.3	769	3	US-08-434-000A-10	Sequence 10, Appl
14	186	5.3	769	4	US-09-312-157-10	Sequence 10, Appl
15	182	5.2	757	3	US-08-434-000A-6	Sequence 6, Appli
16	182	5.2	757	4	US-09-312-157-6	Sequence 6, Appli
17	180.5	5.2	1184	4	US-09-266-225D-18	Sequence 18, Appl
18	178	5.1	1185	3	US-09-041-886-23	Sequence 22, Appl
19	167.5	4.8	624	2	US-08-642-408A-22	Sequence 22, Appl
20	167.5	4.8	624	4	US-09-199-534-22	Sequence 22, Appl
21	167.5	4.8	624	4	US-09-199-534-22	Sequence 22, Appl
22	167.5	4.8	773	3	US-08-434-000A-2	Sequence 2, Appli
23	167.5	4.8	773	4	US-09-312-157-2	Sequence 2, Appli
24	164.5	4.7	589	4	US-09-252-991A-28836	Sequence 28836, A
25	158.5	4.5	657	4	US-09-252-991A-28001	Sequence 28001, A
26	158	4.5	1298	2	US-08-690-473-2	Sequence 2, Appli
27	158	4.5	1298	3	US-09-259-821A-2	Sequence 2, Appli
28	158	4.5	1298	3	US-08-843-659-2	Sequence 2, Appli
29	156.5	4.5	726	4	US-09-252-991A-20675	Sequence 20675, A
30	150.5	4.3	407	4	US-09-252-991A-31517	Sequence 31517, A
31	150.5	4.3	500	4	US-09-252-991A-19739	Sequence 19739, A
32	150	4.3	328	4	US-09-252-991A-21969	Sequence 21969, A
33	148.5	4.3	351	4	US-09-252-991A-18476	Sequence 18476, A
34	148	4.2	774	4	US-09-252-991A-16789	Sequence 16789, A
35	147.5	4.2	826	4	US-09-894-998A-47	Sequence 24254, A
36	147.5	4.2	826	4	US-09-894-998A-47	Sequence 47, Appl
37	146	4.2	355	3	US-08-483-533-41	Sequence 41, Appl
38	146	4.2	355	4	US-09-283-471A-41	Sequence 41, Appl
39	146	4.2	355	5	PCT-US91-06532-3	Sequence 3, Appli
40	146	4.2	638	4	US-09-252-991A-27068	Sequence 27068, A
41	146	4.2	663	4	US-09-252-991A-30843	Sequence 30843, A
42	145	4.2	538	4	US-09-252-991A-32064	Sequence 32064, A
43	144.5	4.1	1520	4	US-09-252-991A-17501	Sequence 17501, A
44	144	4.1	478	4	US-09-252-991A-25191	Sequence 25191, A
45	143.5	4.1	616	4	US-09-252-991A-25638	Sequence 25638, A

ALIGNMENTS

RESULT 1

US-08-961-564A-2

; Sequence 2, Application US/08961564A

; Patent No. 6114515

; GENERAL INFORMATION:

; APPLICANT: WU, SHUJIAN

; APPLICANT: SWEET, RAYMOND

; APPLICANT: TRUNEL, ALEMSEGED

; TITLE OF INVENTION: PIGRL-1, A MEMBER OF IMMUNOGLOBULIN

; TITLE OF INVENTION: GENE SUPERFAMILY

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: RATNER & PRESTIA

; STREET: P.O. BOX 980

; CITY: VALLEY FORGE

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FASTSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/961,564A

; FILING DATE: 30-OCT-1997

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/056,935

; FILING DATE: 25-AUG-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: PRESTIA, PAUL F

; REGISTRATION NUMBER: 23,031

; REFERENCE/DOCKET NUMBER: GH-70236

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-407-0700

TELEFAX: 610-407-0701  
TELEX: 846169  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 390 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-961-564A-2

Alignment Scores:  
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Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 58.91% Indels: 0  
DB: 3 Gaps: 0

US-09-651-150B-1 (1-1911) x US-08-961-564A-2 (1-390)

QY 74 ATGGACTTCTGGCTTGGCCACTTTACTTCTCCAGTATCAGGGCCCTGAGGATCCTC 133  
DB 1 MetAspPheTrpLeuTrpProLeuTyrPheLeuProValSerGlyAlaLeuArgIleLeu 20  
QY 134 CCAGAGTAAGGTAGAGGGGAGCTGGGGGATCAGTTACATCAATGCCACTTCT 193  
DB 21 ProGluValLysValGluGlyLeuGlyGlySerValThrIleLysCysProLeuPro 40  
QY 194 GAAATGCATGCAGATATCTGTCGGGAGATGGCTGGATCTGGACATCTGGTACC 253  
DB 41 GluMetHisValArgIleTyrLeuCysArgGluMetAlaGlySerGlyThrCysGlyThr 60  
QY 254 GTGGTATCCACACCACTTTCATCAAGCAGATAAAGGGCCGAGTTACTCTGAAGCAA 313  
DB 61 ValValSerThrThrAsnPheIleLysAlaGluTyrLysGlyArgValThrLeuLysGln 80  
QY 314 TACCCACGAGAATCTGTTCTAGTGAGGTAAACACAGCTCAGAGAAAGTCACAGCGA 373  
DB 81 TyrProArgLysAsnLeuPheLeuValGluValThrGlnLeuThrGluSerAspSerGly 100  
QY 374 GTCTATGCTGGGAGCGGGCATGAACACAGACCGGGGAAAGACCAAGATCTACCCCTG 433  
DB 101 ValTyrAlaCysGlyAlaGlyMetAsnThrAspArgGlyLysThrGlnLysValThrLeu 120  
QY 434 AATGTCCACAGTGAATACAGCCATCATGGGAGAGCAGCCCAATGCCGTGAGACTCCAAA 493  
DB 121 AsnValHisSerGluTyrGluProSerTrpGluGluGlnProMetProGluThrProLys 140  
QY 494 TGGTTTCATCTCCCTATTTGTTCCAGATGCCGTGATATGCCAGTTCTTCCAAATTCGTA 553  
DB 141 TrpPheHisLeuProTyrLeuPheGlnMetProAlaTyrAlaSerSerLysPheVal 160  
QY 554 ACCAGAGTTACACACCACTCAAGGGGCAAGGTCCTCCAGTTCCACCTCTCCCTCC 613  
DB 161 ThrArgValThrThrProAlaGlnArgGlyLysValProProValHisHisSerPro 180  
QY 614 ACCACCCAAATCACCCAGCCCTCGAGTGTCCAGAGCATCTTCAGTAGCAGGTGACAG 673  
DB 181 ThrThrGlnIleThrHisArgProArgValSerArgAlaSerSerValAlaGlyAspLys 200  
QY 674 CCCGAACTTCTGCTCCACTACAGCTCAAAAATCTCAGCTCTGGAGGGCTGCNC 733  
DB 201 ProArgThrPheLeuProSerThrThrAlaSerLysIleSerAlaLeuGluGlyLeuLeu 220  
QY 734 AAGCCCCAGACGCCAGCTTACACCAACACAGGCTGCACAGGCGAGAGCACTGGAC 793  
DB 221 LysProGlnThrProSerTyrAsnHisHisThrArgLeuHisArgGlnArgAlaLeuAsp 240  
QY 794 TATGGTCACTCTGGGAGGAGGCGCAAGGATTTTCATCTGATCCCGACCATCTCG 853  
DB 241 TyrGlySerGlnSerGlyArgGluGlyGlnGlyPheHisIleLeuIleProThrIleLeu 260

QY 854 GGCCTTTTCTCTGCTGCACCTTCTGGGCTGGTGGTGAAGAAGCGCCGTGAAAGAGGAAA 913  
DB 261 GlyLeuPheLeuLeuAlaLeuLeuGlyLeuValValLysArgAlaValGluArgArgLys 280  
QY 914 GCCCTCTCCAGCGGGCGCGGACTGGCCGTGAGGATCGCGCCCTGAGAGCTCCCAAG 973  
DB 281 AlaLeuSerArgAlaArgArgLeuAlaValArgMetArgAlaLeuGluSerSerGln 300  
QY 974 AGGCCCCGCGGCTCGCGCGACCGCTCCCAAAACACATCTACAGCCCTGCGCGCG 1033  
DB 301 ArgProArgGlySerProArgProArgSerGluAsnAsnIleTyrSerAlaCysProArg 320  
QY 1034 CGCGCTCTGGAGCGAGCTGCAGGCACAGGGAGGCGCCCGTTCGCCGCCCGCGAGCG 1093  
DB 321 ArgAlaArgGlyAlaAspAlaAlaGlyThrGlyGluAlaProValProGlyProGlyAla 340  
QY 1094 CGTTTGGCCCCCGCGCTGCAGGTGTCTGAATCTCCCTGGCTCCATGCCCACTCTCG 1153  
DB 341 ProLeuProProAlaProLeuGlnValSerGluSerProTrpLeuHisAlaProSerLeu 360  
QY 1154 AAGACCAGCTGTGAATACGTGAGCCCTTACCACCGCTGCGCGCCATGATGGAGGACGT 1213  
DB 361 LysThrSerCysGluTyrValSerLeuTyrHisGlnProAlaAlaMetMetGluAspSer 380  
QY 1214 GATTTCAGATGACTACATCAATCTCTCTGCC 1243  
DB 381 AspSerAspAspIleAsnValProAla 390

## RESULT 2

US-09-050-861B-2  
Sequence 2, Application US/09050861B  
Patent No. 6553314  
GENERAL INFORMATION:  
APPLICANT: Payan, Donald  
TITLE OF INVENTION: TOSO AS A TARGET FOR DRUG SCREENING  
FILE REFERENCE: RIGL-002CON  
CURRENT APPLICATION NUMBER: US/09/050,861B  
CURRENT FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: US/09/651,150B  
PRIOR FILING DATE: 2000-08-30  
PRIOR APPLICATION NUMBER: US 09/050,861  
PRIOR FILING DATE: 1998-03-30  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 390  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-050-861B-2

Alignment Scores:  
Pred. No.: 1,37e-167 Length: 390  
Score: 2047.00 Matches: 389  
Percent Similarity: 99.74% Conservative: 0  
Best Local Similarity: 99.74% Mismatches: 1  
Query Match: 58.65% Indels: 0  
DB: 4 Gaps: 0

US-09-651-150B-1 (1-1911) x US-09-050-861B-2 (1-390)

QY 74 ATGGACTTCTGGCTTGGCCACTTTACTTCTCCAGTATCAGGGCCCTGAGGATCCTC 133  
DB 1 MetAspArgTrpLeuTrpProLeuTyrPheLeuProValSerGlyAlaLeuArgIleLeu 20  
QY 134 CCAGAGTAAGGTAGAGGGGAGCTGGGGGATCAGTTACATCAATGCCACTTCTCT 193  
DB 21 ProGluValLysValGluGlyGluLeuGlyGlySerValThrIleLysCysProLeuPro 40  
QY 194 GAAATGCATGCAGGATATCTGTCGGGAGATGGCTGGATCTGGAACATCTGGTACC 253  
DB 41 GluMetHisValArgIleTyrLeuCysArgGluMetAlaGlySerGlyThrCysGlyThr 60  
QY 254 GTGGTATCCACCACTTTCATCAAGGCGAGATAAAGGGCGCGAGTTACTCTGAAGCAA 313

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Db 61 ValValSerThrThrAsnPhelIleLysAlaGluTyrLysGlyArgValThrLeuLysGln 80
QY 314 TACCCACGCAAGATCTGTCTAGTGGAGGTAAACAGCTGACAGAAAGTGACAGCGGA 373
Db 81 TyrProArgLysAsnLeuPheLeuValGluValThrGlnLeuThrGluSerAspSerGly 100
QY 374 GTCTATCGCTCGGAGCGGCATGAACACAGACCGGGGAAGACCCAGAAAGTACCCCTG 433
Db 101 ValTyrAlaCysGlyAlaGlyMetAsnThrAspArgGlyLysThrGlnLysValThrLeu 120
QY 434 AATGTCACAGTGAATACGAGCCATCATGGGAAGACAGCAATGCTGAGACTCCAAAA 493
Db 121 AsnValHisSerGluTyrGluProSerTrpGluGluProMetProGluThrProLys 140
QY 494 TGGTTTCATCTGCCCTATTGTTCAGATCCCTGCATATGCCAGTCTTCCCAATTCGTA 553
Db 141 TrpPheHisLeuProTyrLeuPheGlnMetProAlaTyrAlaSerSerLysPheVal 160
QY 554 ACCAGAGTTACACACAGCTCAAGGGGCAAGTCCCTCCAGTTCACCACTCTCCCCC 613
Db 161 ThrArgValThrThrProAlaGlnArgGlyLysValProProValHisSerSerPro 180
QY 614 ACACCCAAATCACCCACCGCCCTCGAGTGTCCAGAGCATCTTCAGTAGCAGGTGACAAG 673
Db 181 ThrThrGlnIleThrHisArgProArgValSerArgAlaSerSerValAlaGlyAspLys 200
QY 674 CCCGAACCTCTCTGCATCCACTACAGCTCAAAATCTCAAAATCTCAGCTCTGAGGGGCTGCTC 733
Db 201 ProArgThrPheLeuProSerThrThrAlaSerLysIleSerAlaLeuGluGlyLeuLeu 220
QY 734 AAGCCCCAGACCCCGAGCTACACACACACAGCTGCAGAGTGCAGAGGAGAGCAGCTGGAC 793
Db 221 LysProGlnThrProSerThrAsnHisThrArgLeuHisArgGlnArgAlaLeuAsp 240
QY 794 TATGGCTCACGTCTGGAGGAAGCCCAAGGATTCACATCTGATCCGACCATCCCTG 853
Db 241 TyrGlySerGlnSerGlyArgGluGlyGlnGlyPheHisIleLeuIleProThrIleLeu 260
QY 854 GGCCTTTCTCTGCTGCACTCTGGGCTGGTGGTGAAGAGGCGCTTGAAGAGGAGAA 913
Db 261 GlyLeuPheLeuLeuAlaLeuLeuGlyLeuValValLysArgAlaValGluArgArgLys 280
QY 914 GCGCTCTCCAGCGGCGCGGACTGGCGCTGAGATCGCGCGCTGAGAGCTCCCGAG 973
Db 281 AlaLeuSerArgArgAlaArgArgLeuAlaValArgMetArgAlaLeuGluSerSerGln 300
QY 974 AGGCGCGCGGCTCGCGGACCGGCTCCCAAAACACATCTACAGCGCTGCGCGCGG 1033
Db 301 ArgProArgGlySerProArgProArgSerGlnAsnAsnIleTyrSerAlaCysProArg 320
QY 1034 CCGCTCTCGTGGAGCGAGCTGACGACAGGAGGAGCGCGCTTCCCGCGCGCGGAGCG 1093
Db 321 ArgAlaArgGlyAlaAspAlaGlyThrGlyGluAlaProValProGlyProGlyAla 340
QY 1094 CGGTGCGCGCGCGCGCTGCGAGTGTGAATCTCCCTGCTCCATGCCCATCTCTG 1153
Db 341 ProLeuProAlaProLeuGlnValSerGluSerProTrpLeuHisAlaProSerLeu 360
QY 1154 AAGACACAGCTGTGATAGCTGAGCTCTACACAGCGCTGCGCGCATGATGAGGAGACGT 1213
Db 361 LysThrSerCysGluTyrValSerLeuTyrHisGlnProAlaAlaMetMetGluAspSer 380
QY 1214 GATTTCAGATGACTACATCAATCTTCTCCGCC 1243
Db 381 AspSerAspAspTyrIleAsnValProAla 390
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## RESULT 3

US-09-724-864-45  
; Sequence 45, Application US/09724864  
; Patent No. 6380362  
; GENERAL INFORMATION:  
; APPLICANT: Watson, James D

APPLICANT: Murison, James G.  
TITLE OF INVENTION: Polynucleotides, polypeptides expressed  
FILE OF INVENTION: by the polynucleotides and methods for their use.  
FILE REFERENCE: 11000.105001  
CURRENT APPLICATION NUMBER: US/09724,864  
CURRENT FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678  
PRIOR FILING DATE: 1999-12-23  
NUMBER OF SEQ ID NOS: 72  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 45  
LENGTH: 422  
TYPE: PRT  
ORGANISM: Mouse  
US-09-724-864-45

## Alignment Scores:

Pred. No.:	2,41e-94	Length:	422
Score:	1194.50	Matches:	243
Percent Similarity:	68.32%	Conservative:	46
Best Local Similarity:	57.45%	Mismatches:	113
Query Match:	34.23%	Indels:	21
DB:	4	Gaps:	7

US-09-651-150B-1 (1-1911) x US-09-724-864-45 (1-422)

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QY 74 ATGGACTTGTGGCTTTGGCCACTTACTTCTCCAGATATCAGGGGCCCTGAGATCCTC 133
Db 1 MetAspPheTrpLeuThrLeuLeuTyrPheLeuProValSerGlyAlaLeuArgValLeu 20
QY 134 CCAGAAGTAAAGTAGAGGGGAGCTGGCGGATGATGTTACCATCAAAATGCCACTCTCT 193
Db 21 ProGluValGlnLeuAsnValGluTrpGlyGlySerIleIleIleIleIleIleIle 40
QY 194 GAAATCACTGTAGGATATATCTGTCCGGAGATGGCTGGATCTCGAACATGTGTACC 253
Db 41 GlnLeuHisValArgMetTyrLeuCysArgGlnMetAlaLysProGlyIleCysSerThr 60
QY 254 GTGGTATCCACCACTTATCAAGGAGAGTAAACAGGCGGAGTCTACTCTGAAGCAA 313
Db 61 ValValSerAsnThr---PheValLysLysGluTyrGluArgValThrLeuThrPro 79
QY 314 TACCCACGCAAGATCTGTCTAGTGGAGTAAACAGCTGACAGCAAAAGTGACAGCGGA 373
Db 80 CysLeuAspLysLysLeuPheLeuValGluMetThrGlnLeuThrGluAsnAspGly 99
QY 374 GTCTATCGCTCGGAGCGGCATGAACACAGACCGGGGAAGACCCAGAAAGTACCCCTG 433
Db 100 IleTyrAlaCysGlyValGlyMetLysThrAspLysGlyLysThrGlnLysIleThrLeu 119
QY 434 AATGTCACAGTGAATAC---GAGCCATCATGGGAAGACAGCAATGCTGAGATCCTCA 490
Db 120 AsnValHisAsnGluTyrProGluProPheTrpGluAspGluTrpThrSerGluArgPro 139
QY 491 AAATGGTTTCATCTGCCCTATTGTTCCAGATGCCCT-----GCATATGCC 555
Db 140 ArgTrpLeuHisArgPheLeuGlnHisGlnMetProTrpLeuHisGlySerGluHisPro 159
QY 536 AGTTCTTCCAAATTCGTAAACAGAGTTACACACAGCTCAAGAGGCGGAGTCCCTCCA 595
Db 160 SerSerSerGlyValIleAlaLysValThrThrProAlaSerLysThrGluAlaProPro 179
QY 596 GTTCACCACTCTCTCCCGCCACCAACATCAACCCCGCTGAGTGTCCAGAGCATCT 655
Db 180 ValHisGlnProSerSerIleThrSerValThrGlnHisProArgValTyrArgAlaPhe 199
QY 656 TCAGTAGCAGGTGACAAAGCCCGCAACCTTCCCTGCCATCCACTACAGCTCAAAATCTCA 715
Db 200 SerValSerAlaThrLysSerProAlaLeuLeuProAlaThrAlaSerLysThrSer 219
QY 716 GCTCTGGAGGCGCTCTCAAGCCCGCAGAGCGCCAGCTACACACACACAGGCTGAC 775
Db 220 ThrGlnGlnAla---IleArgProLeuGluAlaSerTyrSerHisThrArgLeuHis 238
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Score: 380.00 Matches: 72  
 Percent Similarity: 100.00% Conservative: 1  
 Best Local Similarity: 98.63% Mismatches: 0  
 Query Match: 10.89% Indels: 0  
 DB: 4 Gaps: 0

US-09-651-150B-1 (1-191) x US-09-050-861B-3 (1-73)

QY 170 GTTACATCAATGCCACTTCTCGAATGATGAGGATATATCTGTGCGGGAGATG 229  
 Db 1 ValThrIleLysCysProLeuProGluMetHisValArgIleLysLeuCysArgGluMet 20  
 QY 230 GCTGATCGAATGCGATGGTACCGTGTATCCACCACTTCATCAAGCGCAATAC 289  
 Db 21 AlaGlySerGlyThrCysGlyThrValValSerThrAsnPhelIleLysAlaGluTrp 40  
 QY 290 AAGGCCGAGTACTCTCAAGCAATACCCAGCAGAAATCTGTCTAGTGAGTAACA 349  
 Db 41 LysGlyArgValThrLeuLysGlnTrpProArgLysAsnLeuPheLeuValGluValThr 60  
 QY 350 CAGCTGACAGAAAGTGACAGCGGAGTCTATCGCTCGCGA 388  
 Db 61 GlnLeuThrGluSerAspSerGlyValThrAlaCysGly 73

# RESULT 6

US-09-050-861B-12  
 ; Sequence 12, Application US/09050861B  
 ; Patent No. 6555314  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Payan, Donald  
 ; TITLE OF INVENTION: TOSO AS A TARGET FOR DRUG SCREENING  
 ; FILE REFERENCE: RIGL-002CON  
 ; CURRENT APPLICATION NUMBER: US/09/050.861B  
 ; PRIOR FILING DATE: 1998-03-30  
 ; PRIOR APPLICATION NUMBER: US/09/651.150B  
 ; PRIOR FILING DATE: 2000-08-30  
 ; PRIOR APPLICATION NUMBER: US 09/050.861  
 ; PRIOR FILING DATE: 1998-03-30  
 ; NUMBER OF SEQ ID NOS: 35  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 12  
 ; LENGTH: 43  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens

US-09-050-861B-12  
 Alignment Scores:  
 Pred. No.: 3,75e-12 Length: 43  
 Score: 233.00 Matches: 43  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 6.68% Indels: 0  
 DB: 4 Gaps: 0

US-09-651-150B-1 (1-191) x US-09-050-861B-12 (1-43)

QY 971 CAGAGCGCGGTCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1030  
 Db 1 GlnArgProArgGlySerProArgProArgSerGlnAsnIleLysSerAlaCysPro 20  
 QY 1031 CGCGCGCTCGTGCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1090  
 Db 21 ArgArgAlaArgGlyAlaAspAlaAlaGlyThrGlyAlaProValProGlyProGly 40  
 QY 1091 GCGCGCTTG 1099  
 Db 41 AlaProLeu 43

# RESULT 7

US-09-095-385-4  
 ; Sequence 4, Application US/09095385  
 ; Patent No. 6300104  
 ; GENERAL INFORMATION:

APPLICANT: Morrison, Sherie L.  
 APPLICANT: Chintalacharuvu, Kote R.  
 TITLE OF INVENTION: SECRETORY IMMUNOGLOBULIN PRODUCED  
 BY SINGLE CELLS AND METHODS FOR MAKING AND USING  
 TITLE OF INVENTION: SAME  
 NUMBER OF SEQUENCES: 4  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt  
 STREET: 11150 Santa Monica Boulevard, Suite 400  
 CITY: Los Angeles  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 90025  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/095.385  
 FILING DATE: 09-JUN-1998  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/050.969  
 FILING DATE: 19-JUN-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Canady, Karen S  
 REGISTRATION NUMBER: 39,927  
 REFERENCE/DOCKET NUMBER: 30435.45USU1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 310 445-1140  
 TELEFAX: 310 445-9031  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 608 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: unknown  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-095-385-4

# Alignment Scores:

Pred. No.: 7,52e-09 Length: 608  
 Score: 200.00 Matches: 115  
 Percent Similarity: 35.11% Conservative: 76  
 Best Local Similarity: 21.14% Mismatches: 186  
 Query Match: 5.73% Indels: 167  
 DB: 4 Gaps: 20

US-09-651-150B-1 (1-191) x US-09-095-385-4 (1-608)

QY 79 CTTGCTTGCCACTTTACTTCTGCGGAGTATGCGGCGGCGGCGGCGGCGGCGG 138  
 Db 6 LeuThrCysLeuAlaValPheProAla-IleSerThrLysSerProIlePheGlyPr 25  
 QY 139 AGTAAAGTAGAGGGGAGCTGGCGGATCAGTATACCATCAATGCGCCACTTCT 193  
 Db 25 oGluGluValAsnSerValGluGlyAsnSerValSerIleThrCysTyrTrpPro 45  
 QY 194 -----GAAATGATGTAGGATATATCTGCGGAGATGGCTGGATCTGGAACATG 246  
 Db 45 rSerValAsnArgHisThrArgLysTyrTrpCysArgGlnGlyAlaArgGlyGly 64  
 QY 247 TGGTACCGTGGTATCCACCACCACTTCATCAAGGCAAGATAACAAGGCGGAGTTACTCT 306  
 Db 64 sIleThrLeuIleSerSerGluGlyTyrValSerSerLysTyrAlaGlyArgAlaAsnLe 84  
 QY 307 GAAGCAATACCCACGCAAGAAATCTGTCTTCTAGTGGAGTAACAGCTGACAGAAAGTGA 366  
 Db 84 uThrAsnPheProGluAsnGlyThrPheValValAsnIleAlaGlnLeuSerGlnAspAs 104  
 QY 367 CAGCGGAGTCTATGCTGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 403

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Db 104 pSerGlyArgTyrLysCysGlyLeuGlyIleAsnSerArgGlyLeuSerPheAspValse 124
QY 404 -----GACCG 408
Db 124 rLeuGluValSerGlnGlyProGlyLeuLeuAsnAspThrLysValTyrThrValAspLe 144
QY 409 GGGAAAGACCCAGAAAGTCACTGATGTCACAGTGAATAGAGCAGCATCATGGGAAGA 468
Db 144 uGlyArgThr-----ValThrIleAsnCysProPheLysThrGluAsnAlaGlnLysAr 162
QY 469 GCAGCCACCGCTGAGACTCCAAAATGGTTTCATCTCCCTATTTGTTCCAGATGCTGC 528
Db 162 gLysSerLeuTyrLys-----GlnIleGlyLe 171
QY 529 ATATGCCAGTTCIT-----CCAAATTCGTAACACAGAGT 561
Db 171 uTyr-ProValLeuValIleAspSerSerGlyTyrValAsnProAsnTyrThrGlyArgI 191
QY 562 TACCACACACAGCTCAAGGGCAAGTCCCTCCAGTTCACCACTCCCTCCGCCACCAACCA 621
Db 191 leArgLeuAspIleGlnGlyThrGlyGlnLeuPheSerValValIleAsnGlnLeuA 211
QY 622 AATCACCACCGCTCGAG-----TGT-----CCAG 648
Db 211 rgLeuSerAspAlaGlyGlnTyrLeuCysGlnAlaGlyAspSerAsnSerAsnLysL 231
QY 649 AGCATCTTCACTACGAGTCAAGCCGACAGCTCTCTGCTCCATCCATCAGCTCAAA 708
Db 231 ysAsnAlaAspLeuGlnValLeuLysProGluProGlu-LeuValTyrGluAspLeuArg 250
QY 709 AATCTCAGCTCTGGAGGGCTGCTCAAGCCGCCAGCGCC----- 747
Db 251 GlySerValThrPheHisCysAlaLeuGlyProGluValAlaAsnValAlaLysPheLeu 270
QY 748 -----CAGCTACAAACACACACAGCTCCAGGAGCAGAGCAGTGGCTATGGCTC 801
Db 271 CysArgGlnSerSerGlyGluAsnCysAspValValValValValValValValValVal 290
QY 802 ACAGTCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 861
Db 291 ProAlaPheGluGlyArgIleLeuLeuAsnProGlnAspLysAsp-----GlySerPhe 308
QY 862 CTGCTGCACCTCTGGGGCTGGTGGTGA----- 891
Db 309 SerValValIleThrGlyLeuArgLysGluAspAlaGlyArgTyrLeuCysGlyAlaHis 328
QY 892 ---AAGGCCCTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 948
Db 329 SerAspGlyGlnLeuGlnGlySerProIleGlnAlaTrpGlnLeuPheValAsnGlu 348
QY 949 GATCGCGCCCTGGAGAGCTCCAGAGGCGCGCGGCTCGCGCGCGCGCTCCCAAAA 1008
Db 349 GluSer-----ThrIleProArgSerProThrValVal-LysGlyValAlaGlyse 365
QY 1009 CAACATCTACAGCGCTCGCGCGCGCGCTCGCGCGCTCGCGCGCTCGCGCGCTCGCGCG 1048
Db 365 rSerValAlaValLeuCysProTyrAsnArgLysGluSerLysSerIleLysTyrTrpCy 385
QY 1049 -----CAGCTGCAGGCACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1101
Db 385 sLeuTrpGluGlyAlaGlnAsnGlyArg----- 394
QY 1102 CCGCGCGCGCTGAGGTGTCGATCTCCCTGGCTCCATGCGCCCATCTCTCAAGACCAAG 1161
Db 395 ---CysProLeuLeuValAspSerGluGlyTrpValLysAla----- 407
QY 1162 CTGTGAATAC-----GTGAGCCTCTACACACAGCTGCC----- 1195
Db 408 ----GlnTyrGluGlyArgLeuSerLeuLeuGluGluProGlyAsnGlyThrPheThrVa 426
QY 1195 ----- 1195
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Db 426 lIleLeuAsnGlnLeuThrSerArgAspAlaGlyPheTyrTrpCysLeuThrAsnGlyAs 446

QY 1196 -GCCATGATGAGGACAGACATGATTCAGATGACTATACATCAUGTTCCTGCTGCACACATCCC 1254

Db 446 pThrLeu-TrpArgThrThrValGluIleLys-----IleIleGluGlyGluP 462

QY 1255 CAGCTATCCCCCACCACCCAGCTCGGACTGTGGTGGCCAAAGGAGTCTCATCTATCTGCTGA 1314

Db 462 roAsnLeuLysValProGlyAsnValThrAlaVal-----L 474

QY 1315 TGTCCATACCTGCTTCATGTTCTCAGAGCCCTCATCTCCCATGCCCCCATCTCGA 1374

Db 474 euGlyGluThrLeu-----LysValProCysHisPheProCysLysPheSerS 490

QY 1375 CT 1376

Db 490 er 490

RESULT 8

US-08-434-000A-8

Sequence 8, Application US/08434000A

Patent No. 6046037

GENERAL INFORMATION:

APPLICANT: ANDREW C. HIAIT, JULIAN

APPLICANT: K.-C. MA, THOMAS LEHNER

TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

CITY: Suite 4700

STATE: Los Angeles

COUNTRY: California

COUNTRY: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/434,000A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA: including application

PRIOR APPLICATION DATA: described below: 1

APPLICATION NUMBER: 08/367,395

FILING DATE: 12/30/94

ATTORNEY/AGENT INFORMATION:

NAME: Guise, Jeffrey W.

REGISTRATION NUMBER: 34,613

REFERENCE/DOCKET NUMBER: 212/127

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 552-8400

TELEFAX: (619) 552-0159

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 771 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

DESCRIPTION: Mouse Polyimmunoglobulin Receptor

US-08-434-000A-8

Alignment Scores: 8.28e-09 Length: 771

Pred. No.: 200.00 Matches: 55

Score: 44.57% Conservative: 23

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Best Local Similarity: 31.43% Mismatches: 73
Query Match: 5.73% Indels: 24
DB: 3 Gaps: 5

US-09-651-150b-1 (1-1911) x US-08-434-000A-8 (1-771)
QY 80 TTCTGGCTTTGGCCACTTTACTTCTGCGAGTATCAGGGCCCTGAGGATCCTCCAGAA 139
Db 6 PheThrLeuValThrValPheSerGlyValSerThrLysSerProIlePheGlyPro 25
QY 140 GTAAAGGTAGAGGGGAGCTGGCGGATCAGTACCAATCAATGCCCCTCTCCGAA--- 196
Db 26 GlnGluValSerSerIleGluGlyAspSerValSerIleThrCysTyrTyrProAspThr 45
QY 197 -----ATGCAATGTCAGGATATATCTGTCGGGAGATGCTGGATCTGGAACATGT 247
Db 46 SerValAsnArgHisThrArgLysTyrTrpCysArgGlnGlyAla---SerGlyMetCys 64
QY 248 GGTACCGTGTATGCTCCACCACTTCATCAAGGCGAGATACAGGGCCGAGTACTCTG 307
Db 65 ThrThrLeuIleSerSerAsnGlyTyrLeuSerLysGluTyrSerGlyArgAlaAsnLeu 84
QY 308 AAGCAATACCCACGACAGATCTCTTCTAGTGGAGTAAACAGCTGACAGAAAGTGAC 367
Db 85 IleAsnPheProGluAsnAsnThrPheValIleAsnIleGluGlnLeuThrGluAspAsp 104
QY 368 AGCGGAGTCTATGCTGCGGAGCGGATGACACAGACCGGGGAAAGACCCAGAAAGTC 427
Db 105 ThrGlySerTyrLysCysGlyLeuGly---ThrSerAsnArgGlyLeuSerPheAspVal 123
QY 428 ACCCTGAATGTCACAGTGAATACGACCATCATGGAAGAGAGCAGCCATGCTGAGACT 487
Db 124 SerLeuGluVal-----SerGlnValProGluLeu 133
QY 488 CCAAAATGTTTTCATCTGCCCTATTGTTCCAGATGCTGATGCTGATCTCTCCAAA 547
Db 134 ProSerAspThrHisVal-----TyrThrLysAspIleGly 145
QY 548 TTCGTACACAGATTACACACAGCTCAAGGGGCAAGGTCCT 592
Db 146 ArgAsnValThrIleGluCysProPheLysArgGluAsnValPro 160

RESULT 9
US-09-312-157-8
; Sequence 8, Application US/09312157
; Patent No. 6303341
; GENERAL INFORMATION:
; APPLICANT: ANDREW C. HIATT, JULIAN
; K.-C. MA, THOMAS LEHNER
; TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
; PROTEINS IN PLANTS AND THEIR USES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/312,157
; FILING DATE: 14-May-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/434,000
; FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 34,613
REFERENCE/DOCKET NUMBER: 212/127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 552-8400
TELEFAX: (619) 552-0159
TELEX: 67-351
SEQUENCE LISTING
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 771 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
DESCRIPTION: Mouse Polyimmunoglobulin Receptor
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-312-157-8

Alignment Scores:
Pred. No.: 8,28e-09 Length: 771
Score: 200.00 Matches: 55
Percent Similarity: 44.57% Conservative: 23
Best Local Similarity: 31.43% Mismatches: 73
Query Match: 5.73% Indels: 24
DB: 4 Gaps: 5

US-09-651-150b-1 (1-1911) x US-09-312-157-8 (1-771)
QY 80 TTCTGGCTTTGGCCACTTTACTTCTGCGAGTATCAGGGCCCTGAGGATCCTCCAGAA 139
Db 6 PheThrLeuValThrValPheSerGlyValSerThrLysSerProIlePheGlyPro 25
QY 140 GTAAAGGTAGAGGGGAGCTGGCGGATCAGTACCAATCAATGCCCCTCTCCGAA--- 196
Db 26 GlnGluValSerSerIleGluGlyAspSerValSerIleThrCysTyrTyrProAspThr 45
QY 197 -----ATGCAATGTCAGGATATATCTGTCGGGAGATGCTGGATCTGGAACATGT 247
Db 46 SerValAsnArgHisThrArgLysTyrTrpCysArgGlnGlyAla---SerGlyMetCys 64
QY 248 GGTACCGTGTATGCTCCACCACTTCATCAAGGCGAGATACAGGGCCGAGTACTCTG 307
Db 65 ThrThrLeuIleSerSerAsnGlyTyrLeuSerLysGluTyrSerGlyArgAlaAsnLeu 84
QY 308 AAGCAATACCCACGACAGATCTCTTCTAGTGGAGTAAACAGCTGACAGAAAGTGAC 367
Db 85 IleAsnPheProGluAsnAsnThrPheValIleAsnIleGluGlnLeuThrGluAspAsp 104
QY 368 AGCGGAGTCTATGCTGCGGAGCGGATGACACAGACCGGGGAAAGACCCAGAAAGTC 427
Db 105 ThrGlySerTyrLysCysGlyLeuGly---ThrSerAsnArgGlyLeuSerPheAspVal 123
QY 428 ACCCTGAATGTCACAGTGAATACGACCATCATGGAAGAGAGCAGCCATGCTGAGACT 487
Db 124 SerLeuGluVal-----SerGlnValProGluLeu 133
QY 488 CCAAAATGTTTTCATCTGCCCTATTGTTCCAGATGCTGATGCTGATCTCTCCAAA 547
Db 134 ProSerAspThrHisVal-----TyrThrLysAspIleGly 145
QY 548 TTCGTACACAGATTACACACAGCTCAAGGGGCAAGGTCCT 592
Db 146 ArgAsnValThrIleGluCysProPheLysArgGluAsnValPro 160

RESULT 10
US-08-434-000A-4
; Sequence 4, Application US/08434000A
; Patent No. 6046037
; GENERAL INFORMATION:
; APPLICANT: ANDREW C. HIATT, JULIAN
; K.-C. MA, THOMAS LEHNER
; TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
```

TITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR USES  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/434,000A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA: including application

PRIOR APPLICATION DATA: described below: 1

APPLICATION NUMBER: 08/367,395

FILING DATE: 12/30/94

ATTORNEY/AGENT INFORMATION:

NAME: Guise, Jeffrey W.

REGISTRATION NUMBER: 34,613

REFERENCE/DOCKET NUMBER: 212/127

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 552-8400

TELEFAX: (619) 552-0159

TELEX: 67-3510

SEQUENCE LISTING

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 746 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

DESCRIPTION: Human Polymunoglobulin Receptor

US-08-434-000A-4

#### Alignment Scores:

Pred. No.: 9,96e-09 Length: 746  
Score: 199.00 Matches: 113  
Percent Similarity: 35.21% Conservative: 75  
Best Local Similarity: 21.16% Mismatches: 174  
Query Match: 5.70% Indels: 172  
DB: 3 Gaps: 22

US-09-651-150B-1 (1-1911) x US-08-434-000A-4 (1-746)

QY	107	CCAGTATCAGGGCCCTCAGGATCTCCGAGAAGTAAAGTAGAGGGGAGCTGGCGGA	166
DB	3	ProfilePheGly-----ProGlu-----GluValAsnSerValGluGlyAsn	16
QY	167	TCAGTTACCATCAATGCCACTTCCT-----GAAATGCATGTGAGGATATAT	214
DB	17	SerValSerIleThrCysTyrTyrProProThrSerValAsnArgHisThrArgIysTyr	36
QY	215	CTGTCCGGGAGATCGTGGATCTGGAACATGTGTACCGTGGTATCCACCAACTTC	274
DB	37	TrpCysArgGlnGlyAlaArgGlyGly---CysIleThrLeuIleSerSerGluGlyTyr	55
QY	275	ATCAAGGAGGAATCAAGGGCCAGTTACTCTGAAGCAATACCCACGAAGAATCTGTTT	334
DB	56	ValSerSerIleTyrAlaGlyArgAlaAsnLeuThrAsnPheProGluAsnGlyThrPhe	75
QY	335	CTAGTGGAGGTAAACAGCTGACAGAAAGTACACGGAGTCTATGCTCGGAGCGGGC	394
DB	76	ValValAsnIleAlaGlnLeuSerGlnAspSerGlyArgTyrIysCysGlyLeuGly	95

QY	395	ATGAACACA-----	403
DB	96	IleAsnSerArgGlyLeuSerPheAspValSerLeuGluValSerGlnGlyProGlyLeu	115
QY	404	-----GACCGGGGAAGACCCAGAAAGTCACCTGAAT	436
DB	116	LeuAsnAspThrLysValTyrThrValAspLeuGlyArgThr-----ValThrIleAsn	133
QY	437	GTCCACAGTGAATACGACCCATCATGGGAGAGCAGCAATGCCTGAGACTCCAAATGG	496
DB	134	CysProPheLysThrGluAsnAlaGlnLysArgLysSerLeuTyrLys-----	149
QY	497	TTTCATCTGCCCTATTTCCTCCAGATGCCTGCATATGCCAGTTCCT	542
DB	150	-----GlnIleGlyLeuTyr-ProValLeuValIleAspSerSe	162
QY	543	-----CCAAATTCGTACACAGAGTATCCACACACAGCTCAAGGGGCAAGGTC	589
DB	162	rGlyTyrValAsnProAsnTyrThrGlyArgIleArgLeuAspIleGlnGlyThrGlyG1	182
QY	590	CTCCAGTTCACCACTCCTCCCCACACCCCAATACCCACCGCCCTCGAG-----TG	643
DB	182	nLeuLeuPheSerValValIleAsnGlnLeuArgLeuSerAspAlaGlyGlnTyrLeuCy	202
QY	644	T-----CCAGAGCATCTTCAGTAGCAGGTACACAGGCC	676
DB	202	sglnAlaGlyAspSerAsnSerAsnLysLysAsnAlaAspLeuGlnValLeuLysPr	222
QY	677	CGAACCTTCCTGCCATCCACTACAGCCTCAAAATCTCAGCTCTGGAGGGCTGCTCAAG	736
DB	222	oGluProGlu-LeuValTyrGluAspLeuArgGlySerValThrPheHisCysAlaLeuG	242
QY	737	CCCCAGAGGCC-----CAGCTACACCAACCAACCCAGG	769
DB	242	lyProGluValAlaAsnValAlaLysPheLeuCysArgGlnSerSerGlyGluAsnCysA	262
QY	770	CTGCACAGCAGAGACACTGGACTATGCCTACAGTCTGGGAGGAGGCCAAGATT	829
DB	262	spValValValAsnThrLeuGlyLysArgAlaProAlaPheGluGlyArgIleLeuLeuA	282
QY	830	CACATCTCTGATCCCGACCATCCTGGGCCTTTCTCTGCTGGCACTTCTGGGGCTGGTGG	889
DB	282	snProGlnAspLysAsp-----GlySerPheSerValValIleThrGlyLeuArgLysG	300
QY	890	AA-----AAGGCCGTTGAAAGAGGAAGCC	916
DB	300	IuAspAlaGlyArgTyrLeuCysGlyAlaHisSerAspGlyGlnLeuGlnGlySerP	320
QY	917	CTCTCAGCGGGCGCGCGCGCTGGCGCTGGAGTGGCGCGCTGGAGAGCTCCAGAGG	976
DB	320	toileGluAlaTrpGlnLeuPheValAsnGluGluSer-----ThrIleProArgS	337
QY	977	CCCCCGGGTCCCGCGCGCTCCCAACACATCTACAGCGCTGCCCGCGCGCGC	1036
DB	337	exProThrValVal-LysGlyValAlaGlySerSerValAlaValLeuCysProTyrAsn	356
QY	1037	GCTCGTGGAGCG-----GACGCTGACGGCACAGGGAG	1069
DB	357	ArgLysGluSerLysSerIleLysTyrTrpCysLeuTrpGluGlyAlaGlnAsnGlyArg	376
QY	1070	GCCCCCGTTCGCCGGCGCGGCGCTTGCCTCCCGCGCGCTCGAGTGTCTGAACT	1129
DB	377	-----CysProLeuLeuValAspSerGlu	384
QY	1130	CCCTGGCTCCATGCCCATCTCTGAAGACCACTGTGATAC-----GTGAGCCNC	1180
DB	385	GlyTyrValLysAla-----GlnTyrGluGlyArgLeuSerLeu	397
QY	1181	TACCACACGCTGCC-----	1195
DB	398	LeuGluGluProGlyAsnGlyThrPheThrValIleLeuAsnGlnLeuThrSerArgAsp	417
QY	1196	-----GCCATGATGGAGGACAGTGTATCAGAT	1222

DB 418 AlaGlyPheTyrTrpCysLeuThrAsnGlyAspThrLeu-TpArgIhrThrValGluI 437  
 QY 1223 GACTACATCAATGTCCTGACAACTCCCGACGTAATCCCAACCCAGGTCGGAC 1282  
 DB 437 elys-----IleIleGluGlyGluProAsnLeuLysValProGlyAsnValTh 453  
 QY 1283 TGTGTGCAAGAGAGTCTCATCTATCTGCTGATGTCACAAATACCTGCTTCAITGTTCTCA 1342  
 DB 453 ralaVal-----LeuGlyGluThrLeu-----Ly 461  
 QY 1343 GAGCCCTCATCACTCCCATGCCCATCGCACT 1376  
 DB 461 sValProCysHisPheProCysLysPheSerSer 472

RESULT 11

US-09-312-157-4  
 ; Sequence 4, Application US/09312157  
 ; Patent No. 6303341  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ANDREW C. HIATT, JULIAN  
 ; K.-C. MA, THOMAS LEHNER  
 ; TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION  
 ; PROTEINS IN PLANTS AND THEIR USES  
 ; NUMBER OF SEQUENCES: 19  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Lyon & Lyon  
 ; STREET: 633 West Fifth Street  
 ; Suite 4700  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: U.S.A.  
 ; ZIP: 90071  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0  
 ; SOFTWARE: Word Perfect 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/312,157  
 ; FILING DATE: 14-May-1999  
 ; CLASSIFICATION DATA:  
 ; APPLICATION NUMBER: 08/434,000  
 ; FILING DATE: <Unknown>  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Guise, Jeffrey W.  
 ; REGISTRATION NUMBER: 34,613  
 ; REFERENCE/DOCKET NUMBER: 212/127  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (619) 552-8400  
 ; TELEFAX: (619) 552-0159  
 ; TELEX: 67-351  
 ; SEQUENCE LISTING  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 746 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; DESCRIPTION: Human Polyimmunoglobulin Receptor  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 4

Alignment Scores:  
 Pred. No.: 9,96e-09  
 Score: 199.00  
 Percent Similarity: 35.21%  
 Best Local Similarity: 21.16%  
 Query Match: 5.70%  
 DB: 4

Length: 746  
 Matches: 113  
 Conservative: 75  
 Mismatches: 174  
 Indels: 172  
 Gaps: 22

US-09-651-150B-1 (1-1911) x US-09-312-157-4 (1-746)  
 QY 107 CCAGTATCAGGGCCCTGAGGATCTCCAGAAAGTAAGGTAGAGGGGAGCTGGCGGA 166  
 DB 3 ProIlePheGly-----ProGlu---GluValAsnSerValGluGlyAsn 16  
 QY 167 TCAGTTACATCAAAATGCGCCACTTCCT-----GAAATGCATGTGAGGATATAT 214  
 DB 17 SerValSerIleThrCysTyrTyrProThrSerValAsnArgHisThrArgLysTyr 36  
 QY 215 CTGTCCGGAGATGGCTGATCGTAACATGTGTCAGCGTGTGTTATCCACCAACACATC 274  
 DB 37 TrpCysArgGlnGlyAlaArgGlyGly---CysIleThrLeuIleSerSerGluGlyTyr 55  
 QY 275 ATCAAGCGAGATAACAGGGCGCGAGTTACTCTGAAGCAATACCCACGCAAGAATCTGTC 334  
 DB 56 ValSerSerLysTyrAlaGlyArgAlaAsnLeuThrAsnPheProGluAsnGlyThrPhe 75  
 QY 335 CTAGTGGAGTAACACAGCTGACAGAAAGTGCACGGGAGTCTATGCTCGGGAGCGGC 394  
 DB 76 ValValAsnIleAlaGlnLeuSerGlnAspSerGlyArgTyrLysCysGlyLeuGly 95  
 QY 395 ATGAACACA----- 403  
 DB 96 IleAsnSerArgGlyLeuSerPheAspValSerLeuGluValSerGlnGlyProGlyLeu 115  
 QY 404 -----GACCGGGAAAGACCCAGAAAGTCAACCTGAAT 436  
 DB 116 LeuAsnAspThrLysValTyrThrValAspLeuGlyArgThr-----ValThrIleAsn 133  
 QY 437 GTCCACAGTGAATACGAGCCCATCATGGGAAGAGACAGCAATGCTCGGAGACTCCAAATGG 496  
 DB 134 CysProPheLysThrGluAsnAlaGlnLysArgLysSerLeuTyrLys----- 149  
 QY 497 TTTCATCTGCCCTATTGTTCCAGATGCTCATGCTGCTTCTT----- 542  
 DB 150 -----GlnIleGlyLeuTyr-ProValLeuValIleAspSerSe 162  
 QY 543 -----CCAAATTCGTAAACAGAGTTACACACAGCTCAAGGCGGCAAGTGC 589  
 DB 162 rGlyTyrValAsnProAsnTyrThrGlyArgIleArgLeuAspIleGlnGlyThrGlyG1 182  
 QY 590 CTTCCAGTTCACCACTCTCTCCCGACCAACCAATCACCACCGCCCTCGAG-----TG 643  
 DB 182 nLeuLeuPheSerValValIleAsnGlnLeuArgLeuSerAspAlaGlyGlnLyrLeuCy 202  
 QY 644 T-----CCAGACGATCTTCAGTAGCAGGTGACAGGCC 676  
 DB 202 sGlnAlaGlyAspAspSerAsnSerAsnLysLysAsnAlaAspLeuGlnValLeuLysPr 222  
 QY 677 CGAACCTTCTGCTGCTACAGCTCAAAATCTCAGCTCTGAGGGGCTGCTCAAG 736  
 DB 222 oGluProGlu-LeuValTyrGluAspLeuArgLysSerValThrPheHisCysAlaLeuG 242  
 QY 737 CCCAGACGCGC-----CAGCTACACACCAACACAGG 769  
 DB 242 lyProGluValAlaAsnValAlaLysPheLeuCysArgGlnSerSerGlyLeuAsnCysA 262  
 QY 770 CTGCACAGGAGAGACACTGGACTATGGCTCACAGCTCGGAGGAGGCAAGGATTT 829  
 DB 262 spValValValAsnThrLeuGlyLysArgAlaProAlaPheGluGlyArgIleLeuLeuA 282  
 QY 830 CACATCTGATCCCGACCATCTCTGGGCTTTCTCTGCTGCACTTCTGGGGCTGTGGT 889  
 DB 282 snProGlnAspLysAsp-----GlySerPheValValIleThrGlyLeuArgLysG 300  
 QY 890 AA-----RAGGCGCTTGAAGAGAGAGAGGCC 916  
 DB 300 luAspAlaGlyArgTyrLeuCysGlyAlaHisSerAspGlyGlnLeuGlnGluGlySerP 320  
 QY 917 CTCTCCAGGCGGCGCGCGGCGGCTGAGTGGCGCGCTGAGAGACTCCACAGG 976  
 DB 320 rolleGlnAlaTrpGlnLeuPheValAsnGluGluSer-----ThrIleProArgS 337





Db 68 eSerSerAsnGlyTyrLeuSerLysGlyTyrSerGlyArgAlaSerLeuLeuAsnPhePr 88  
QY 319 ACCCAAGAATCTCTCTAGTGGAGTAACACAGCTGACAGAAAGTGACAGCGAGTCTA 378  
Db 88 oGluAsnSerThrPheValIleAsnIleAlaHisLeuThrGlnGluAspThrGlySerTy 108  
QY 379 TGCTCGGAGCGGCGATGAACACAGACCGGGGAAAGACCCAGAAAGTCAACCTGAATGT 438  
Db 108 rLysCysGlyLeuGly---ThrThrAsnArgGlyLeuPhePheAspValSerLeuGluVa 127  
QY 439 CCACAGTGAATACAGCCATCATGGGAAGACGACCAATGCCGACACATCCAAATGGT 498  
Db 127 l-----SergInValProGluPheProAsnAspTh 137  
QY 499 TCATCTG 505  
Db 137 rHisVal 139

## RESULT 15

US-08-434-000A-6

; Sequence 6, Application US/08434000A

; Patent No. 6046037

## GENERAL INFORMATION:

; APPLICANT: ANDREW C. HIATT, JULIAN

; APPLICANT: K.-C. MA, THOMAS LEHNER

; TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION

; TITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR USES

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon &amp; Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071

## COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/434,000A

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; PRIOR APPLICATION DATA: including application 1

; PRIOR APPLICATION DATA: described below:

; APPLICATION NUMBER: 08/367,395

; FILING DATE: 12/30/94

; ATTORNEY/AGENT INFORMATION:

; NAME: Guise, Jeffrey W.

; REGISTRATION NUMBER: 34,613

; REFERENCE/DOCKET NUMBER: 212/127

; TELEPHONE: (619) 552-8400

; TELEFAX: (619) 552-0159

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 757 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; TOPOLOGY: DESCRIPTION: Bovine Polyimmunoglobulin Receptor

US-08-434-000A-6

## Alignment Scores:

Pred. No.:	2.89e-07	Length:	757
Score:	182.00	Matches:	42



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 13, 2003, 23:38:04 ; Search time 124 Seconds  
(without alignments)  
6802.284 Million cell updates/sec

Title: US-09-651-150B-1

Perfect score: 1911

Sequence: 1 aaaggagtaagcagcgtgctc.....ttactctgtctcctcttt 1911

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_NA:\*

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2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq.\*

3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq.\*

4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq.\*

5: /cgn2\_6/ptodata/2/ina/PCUS\_COMB.seq.\*

6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1911	100.0	1911	4	US-09-050-861B-1
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3	676	35.4	1047	3	US-08-961-564A-3
4	563.6	29.5	1480	4	US-09-724-864-11
5	56.2	2.9	7218	1	US-08-232-463-14
6	48.2	2.5	2430	4	US-09-232-160-16
7	43.4	2.3	7218	1	US-08-232-463-14
8	41.8	2.2	1433	2	US-08-666-392A-1
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10	40.8	2.1	152331	3	US-09-128-155-16
11	40.6	2.1	7812	3	US-09-368-590-1
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13	39.2	2.1	1131	4	US-09-252-991A-1675
14	39.2	2.1	1671	4	US-09-252-991A-1539
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17	37	1.9	429	4	US-09-252-991A-15260
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23	36.6	1.9	1515	1	US-08-221-750A-4
24	36.6	1.9	2571	4	US-09-984-880-1
25	36.6	1.9	7742	1	US-08-221-750A-1
26	36.6	1.9	20966	4	US-09-984-880-3
27	36.4	1.9	672	4	US-09-565-808-3

28	36.4	1.9	1044	1	US-07-975-526-3	Sequence 3, Appli
29	36.4	1.9	1044	4	US-07-974-409C-425	Sequence 425, App
30	36.4	1.9	1929	5	PCT-US93-00031-18	Sequence 18, Appl
31	36.4	1.9	1932	5	PCT-US93-00031-20	Sequence 20, Appl
32	36.4	1.9	1935	4	US-09-620-312D-236	Sequence 236, App
33	36.4	1.9	1941	5	PCT-US93-00031-10	Sequence 10, Appl
34	36.4	1.9	1941	5	PCT-US93-00031-22	Sequence 22, Appl
35	36.4	1.9	2205	5	PCT-US93-00031-12	Sequence 12, Appl
36	36.4	1.9	2208	5	PCT-US93-00031-14	Sequence 14, Appl
37	36.4	1.9	2217	5	PCT-US93-00031-8	Sequence 8, Appl
38	36.4	1.9	2220	5	PCT-US93-00031-16	Sequence 16, Appl
39	36.4	1.9	2811	4	US-08-482-073-3	Sequence 3, Appl
40	36.4	1.9	2813	2	US-08-344-155C-99	Sequence 99, Appl
41	36.4	1.9	2813	4	US-09-009-490A-90	Sequence 90, Appl
42	36.4	1.9	3080	4	US-08-482-073-4	Sequence 4, Appl
43	36.4	1.9	3332	4	US-09-423-890-11	Sequence 11, Appl
44	36.2	1.9	990	4	US-09-252-991A-1499	Sequence 1499, Ap
45	36.2	1.9	1260	4	US-09-252-991A-13265	Sequence 13265, A

## ALIGNMENTS

### RESULT 1

US-09-050-861B-1

; Sequence 1, Application US/09050861B

; Patent No. 6555314

; GENERAL INFORMATION:

; APPLICANT: Payan, Donald

; TITLE OF INVENTION: TOSO AS A TARGET FOR DRUG SCREENING

; FILE REFERENCE: RIGL-002CON

; CURRENT APPLICATION NUMBER: US/09/050,861B

; CURRENT FILING DATE: 1998-03-30

; PRIOR APPLICATION NUMBER: US/09/651,150B

; PRIOR FILING DATE: 2000-08-30

; PRIOR APPLICATION NUMBER: US 09/050,861

; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 1

; LENGTH: 1911

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-050-861B-1

Query Match	100.0%	Score 1911;	DB 4;	Length 1911;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1911;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	AAAGGAGTAAGCAGCGTGTCTCCATCCCTCTTAGGGCTCTTGGAGTGGACCTTGCAC	60	
Db	1	AAAGGAGTAAGCAGCGTGTCTCCATCCCTCTTAGGGCTCTTGGAGTGGACCTTGCAC	60	
Qy	61	TCTAAGAGGACAATGGACTTCTGGCTTTGGCCACTTTACTTCTCTGCGAGTATCAGGGGC	120	
Db	61	TCTAAGAGGACAATGGACTTCTGGCTTTGGCCACTTTACTTCTCTGCGAGTATCAGGGGC	120	
Qy	121	CCTGAGATCTCCCAAGTAAGGTAGAGGGGAGCTGGCGGATCAGTTACATCA	180	
Db	121	CCTGAGATCTCCCAAGTAAGGTAGAGGGGAGCTGGCGGATCAGTTACATCA	180	
Qy	181	ATGCGCACTTCTCAAAATGATGTAGATATCTGTGGCGGAGATGCTGGATCTGG	240	
Db	181	ATGCGCACTTCTCAAAATGATGTAGATATCTGTGGCGGAGATGCTGGATCTGG	240	
Qy	241	AACATGTGGTACCGTGGTATCCACCACTTCCATCAAGGCAATACAAAGGCGGAGT	300	
Db	241	AACATGTGGTACCGTGGTATCCACCACTTCCATCAAGGCAATACAAAGGCGGAGT	300	
Qy	301	TACTTCTGAAGCAATACCCAGCAAGATCTTCTAGTGGAGTAAACAGCTGACAGA	360	
Db	301	TACTTCTGAAGCAATACCCAGCAAGATCTTCTAGTGGAGTAAACAGCTGACAGA	360	



Query Match  
Best Local Similarity 96.4%; Score 1842.4; DB 3; Length 2040;  
Matches 1894; Conservative 0; Mismatches 11; Indels 5; Gaps 4;  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-961-564A-1

QY 5 GAGTAAGCAGGTGCTCCATCCCTCTCTAGGGGCTCTTGGATGACCTTGCACTCTA 64  
Db |||||||  
QY 77 GAGTAAGCAGGTGCTCCATCCCTCTCTAGGGGCTCTTGGATGACCTTGCACTCTA 136  
Db |||||||  
QY 65 GAAGGGACAATGGACTTCTGGCTTGGCCACTTACTTCTGCGGAGATGCGATGCAATGTC 124  
Db |||||||  
QY 137 GAAGGGACAATGGACTTCTGGCTTGGCCACTTACTTCTGCGGAGATGCGATGCAATGTC 196  
Db |||||||  
QY 125 AGGATCCTCCAGAAAGTAAGGTAGAGGGGAGCTGGCGGATCAGTTACCATCAATGTC 184  
Db |||||||  
QY 197 AGGATCCTCCAGAAAGTAAGGTAGAGGGGAGCTGGCGGATCAGTTACCATCAATGTC 256  
Db |||||||  
QY 185 CCATCTCCTCAAAATGCAATGAGGATATATCTGTGCGGGAGATGCGTGGATCTGGAACA 244  
Db |||||||  
QY 257 CCATCTCCTCAAAATGCAATGAGGATATATCTGTGCGGGAGATGCGTGGATCTGGAACA 316  
Db |||||||  
QY 245 TGTGGTACCGTGTATCCACCACTTCCATCAAGGCAGAAATACAAAGGCCCGAGTTACT 304  
Db |||||||  
QY 317 TGTGGTACCGTGTATCCACCACTTCCATCAAGGCAGAAATACAAAGGCCCGAGTTACT 376  
Db |||||||  
QY 305 CTGAAGCAATPACCCAGCAGAAATCTGTTCCTAGTGGAGGTAAACACAGCTGACAGAAAT 364  
Db |||||||  
QY 377 CTGAAGCAATPACCCAGCAGAAATCTGTTCCTAGTGGAGGTAAACACAGCTGACAGAAAT 436  
Db |||||||  
QY 365 GACAGCGGAGTCTATGCTCGGAGCGGCATGAACACAGACCGGGGAAAGACCCAGAAA 424  
Db |||||||  
QY 437 GACAGCGGAGTCTATGCTCGGAGCGGCATGAACACAGACCGGGGAAAGACCCAGAAA 496  
Db |||||||  
QY 425 GTCACCCCTGAATCTCCACAGTGAATACAGGCCATCATGGAAGAGCAGCCAAATGCCGTGAG 484  
Db |||||||  
QY 497 GTCACCCCTGAATCTCCACAGTGAATACAGGCCATCATGGAAGAGCAGCCAAATGCCGTGAG 556  
Db |||||||  
QY 485 ACTCCAAATGTTTCATCTGCTGCTATTTGTTCCAGATGCTCATATGCGCACTTCTTCC 544  
Db |||||||  
QY 557 ACTCCAAATGTTTCATCTGCTGCTATTTGTTCCAGATGCTCATATGCGCACTTCTTCC 616  
Db |||||||  
QY 545 AAATTCGTAACCAAGAGTATACCAACAGCTCAAGAGGGCAAGTCCCTCCAGTTACCAAC 604  
Db |||||||  
QY 617 AAATTCGTAACCAAGAGTATACCAACAGCTCAAGAGGGCAAGTCCCTCCAGTTACCAAC 676  
Db |||||||  
QY 605 TCCCTCCCCACCAACCAATACCCACCGCTCGAGTGTCCAGAGCATCTTCAGTAGCA 664  
Db |||||||  
QY 677 TCCCTCCCCACCAACCAATACCCACCGCTCGAGTGTCCAGAGCATCTTCAGTAGCA 736  
Db |||||||  
QY 665 GGTGACAAAGCCGGAACCTTCTGCTGCTATCTAGCTCAAAATCTCAGCTCTGAG 724  
Db |||||||  
QY 737 GGTGACAAAGCCGGAACCTTCTGCTGCTATCTAGCTCAAAATCTCAGCTCTGAG 796  
Db |||||||  
QY 725 GGGCTGCTCAAGCCGAGAGCCAGCTACACCAACCAACAGGCTGACAGGCAAGCA 784  
Db |||||||  
QY 797 GGGCTGCTCAAGCCGAGAGCCAGCTACACCAACCAACAGGCTGACAGGCAAGCA 856  
Db |||||||  
QY 785 GCAGTGGACTATGGCTCAGAGTCTGGAGGGAGGCAAGGATTTTCACATCTCTGATCCCG 844  
Db |||||||  
QY 857 GCAGTGGACTATGGCTCAGAGTCTGGAGGGAGGCAAGGATTTTCACATCTCTGATCCCG 916  
Db |||||||  
QY 845 ACCATCTGGGCTTTTCTGCTGCTGCTCTGAGGCTGCTGAGGAAAGGCGCGTTGAA 904  
Db |||||||  
QY 917 ACCATCTGGGCTTTTCTGCTGCTGCTCTGAGGCTGCTGAGGAAAGGCGCGTTGAA 976  
Db |||||||  
QY 905 AGGAGGAAAGCCCTCTCCAGGCGGCGCCCGACCTGCGGCTGAGGATGCGCGCCGAG 964  
Db |||||||  
QY 977 AGGAGGAAAGCCCTCTCCAGGCGGCGCCCGACCTGCGGCTGAGGATGCGCGCCGAG 1036  
Db |||||||

## RESULT 3

US-08-961-564A-3

; Sequence 3, Application US/08961564A

; Patent No. 6114515

; GENERAL INFORMATION:

; APPLICANT: WU, SHUJIAN

; APPLICANT: SWEET, RAYMOND

QY 965 AGCTCCAGAGCCCGCGGGGTGCGCGGACCGGCTCCCAAAACACATCTACAGCC 1024  
Db |||||||  
QY 1037 AGCTCCAGAGCCCGCGGGTCCGCGGACCGGCTCCCAAAACACATCTACAGCC 1096  
Db |||||||  
QY 1025 TGCCCGGGCGGCTCGTGGAGGAGGAGCTCGAGGACAGGGAGGCGCCGCTTCCCGGC 1084  
Db |||||||  
QY 1097 TGCCCGGGCGGCTCGTGGAGGAGGAGCTCGAGGACAGGGAGGCGCCGCTTCCCGGC 1156  
Db |||||||  
QY 1085 CCGGAGCGCGGTTCGCCCGCGCGCTGCGAGGTGCTGAATCTCCCTGCGCTCCATGCC 1144  
Db |||||||  
QY 1157 CCGGAGCGCGGTTCGCCCGCGCGCTGCGAGGTGCTGAATCTCCCTGCGCTCCATGCC 1216  
Db |||||||  
QY 1145 CCATCTCTGAAGACAGCTGTGAATAGCTGAGCCCTTACCACAGCCCTCCCGCATGATG 1204  
Db |||||||  
QY 1217 CCATCTCTGAAGACAGCTGTGAATAGCTGAGCCCTTACCACAGCCCTCCCGCATGATG 1276  
Db |||||||  
QY 1205 GAGGACAGTGTAGTACATCAATGTTCTGCTGCTGACAACTCCCGCATGATGCC 1264  
Db |||||||  
QY 1277 GAGGACAGTGTAGTACATCAATGTTCTGCTGCTGACAACTCCCGCATGATGCC 1336  
Db |||||||  
QY 1265 CCAACCCAGGCTCGGACTGTGTGTCGCAAGGAGTCTCATCTATCTGCTGATGCCAATAC 1324  
Db |||||||  
QY 1337 CCAACCCAGGCTCGGACTGTGTGTCGCAAGGAGTCTCATCTATCTGCTGATGCCAATAC 1396  
Db |||||||  
QY 1325 CTGCTTCATGTGTCTCAGAGCCCTCATCTCCCATGCGCCCATCTCGACTCCCATGCC 1384  
Db |||||||  
QY 1397 CTGCTTCATGTGTCTCAGAGCCCTCATCTCCCATGCGCCCATCTCGACTCCCATGCC 1456  
Db |||||||  
QY 1385 CATCTATCTGTGCGCCCTGAGCATGGCTTGCCTCCAGGTGCTGTCGACACCTTGGCAGC 1444  
Db |||||||  
QY 1457 CATCTATCTGT-GCCCTGAGCATGGCTTGCCTCCAGGTGCTGTCGACACCTTGGCAGC 1515  
Db |||||||  
QY 1445 CCCTCTGAGTGTACAGGTAAAGCTGTAGGCAATGTAGAGCAATGTGCCAATGCCACTGCT 1504  
Db |||||||  
QY 1516 CCCTCTGAGTGTACAGGTAAAGCTGTAGGCAATGTAGAGCAATGTGCCAATGCCACTGCT 1575  
Db |||||||  
QY 1505 TCCTTTCCAAAGCGTCCAAAGAGCTGTGGATTTGAGAGGTGTTCTTCCATGCTTTGA 1564  
Db |||||||  
QY 1576 TCCTTTCCAAAGCGTCCAAAGAGCTGTGGATTTGAGAGGTGTTCTTCCATGCTTTGA 1635  
Db |||||||  
QY 1565 CCACAGGCTGTGTTGCTGCGAGGCTTAGATCACATGCGCATGAGGTGGGCGAGGCA 1624  
Db |||||||  
QY 1636 CCACAGGCT-TGTTGCTGCGGAGCTTAGATCACATGCGCATGAGGTGGGCGAGGCA 1694  
Db |||||||  
QY 1625 TAGCTATGCTCTCGGCAAT-CCCTCCAGGTTGGGCTTTACACAAATAGAAGGCTCTTG 1683  
Db |||||||  
QY 1695 TAGCTATGCTCTCGGCAATCCCTTCCAGGTTGGGCTTTACACAAATAGAAGGCTCTTG 1754  
Db |||||||  
QY 1684 CTCTGAGTTATGTCAGCTGCTCAGCCCATGAGCTAAGCAGGCTGCTGGTAT--AAACA 1741  
Db |||||||  
QY 1755 CTCTGAGTTATGTCAGCTGCTCAGCCCATGAGCTAAGCAGGCTGCTGGTATATAAACA 1814  
Db |||||||  
QY 1742 CTCTGAGGAGGCTTTGCGCTGATCCAAATGTAGCAGTGTAGTGAACGCTTACTTA 1801  
Db |||||||  
QY 1815 CTCTGAGGAGGCTTTGCGCTGATCCAAATGTAGCAGTGTAGTGAACGCTTACTTA 1874  
Db |||||||  
QY 1802 TCTCAAGTCTATGCTAAAGGCAATTTATCTTGATGTGATGATAAACAACCTTATAGC 1861  
Db |||||||  
QY 1875 TCTCAAGTCTATGCTAAAGGCAATTTATCTTGATGTGATGATAAACAACCTTATAGC 1934  
Db |||||||  
QY 1862 AGATATGATATATATCCATAAATTTCTTTTACTCTGCTCCATCCTTT 1911  
Db |||||||  
QY 1935 AGATATGATATATATATCCATAAATTTCTTTTACTCTGCTCCATCCTTT 1984  
Db |||||||

```

; APPLICANT: TRUNEH, ALEMSEGED
; TITLE OF INVENTION: PIGRL-1, A MEMBER OF IMMUNOGLOBULIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,564A
; FILING DATE: 30-OCT-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/056,935
; FILING DATE: 25-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70236
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1047 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-961-564A-3

Query Match 35.4%; Score 676; DB 3; Length 1047;
Best Local Similarity 94.6%; Pred. No. 7.6e-193;
Matches 785; Conservative 0; Mismatches 34; Indels 11; Gaps 8;

QY 5 GAGTAAGCAGCGTCTCCATCCCTCTCTAGGGGCTCTTGGATGGACCTTGACACTA 64
DB 11
DB 81 GAGTAAGCAGCGTCTCCATCCCTCTCTAGGGGCTCTTGGATGGACCTTGACACTA 140
QY 65 GAAGGGACAATGACITCTGGCTTTGCCACTTTACTTCTGCCAGTATCAGGGCCCTG 124
DB 141 GAAGGGACAATGACITCTGGCTTTGCCACTTTACTTCTGCCAGTATCAGGGCCCTG 200
QY 125 AGGATCTCCAGAGTAAGGTAGAGGGGAGCTGGCGGATCAGTTACCATCAAAATGC 184
DB 201 AGGATCTCCAGAGTAAGGTAGAGGGGAGCTGGCGGATCAGTTACCATCAAGTC 260
QY 185 CCATCTCCTGAAATGCAATGATGATATCTGTCCGGGAGATGCGTGGATCGGAACA 244
DB 261 CCATCTCCTGAAATGCAATGATGATATCTGTCCGGGAGATGCGTGGATCGGAACA 320
QY 245 TGTGGTACCGTGTATCCACCACCACTTCATCAAGCAGATACAAAGGCGCGAGTTACT 304
DB 321 TGTGGTACCGTGTATCCACCACCACTTCATCAAGCAGATACAAAGGCGCGAGTTACT 380
QY 305 CTGAAGCAATACCCACGCAAGAACTGTCTCTAGTGGAGTAAACACAGCTGACAGAA 364
DB 381 CTGAAGCAATACCCACGCAAGAACTGTCTCTAGTGGAGTAAACACAGCTGACAGAA 440
QY 365 GACAGCGAGTCTATGCTCGGAGCGGGGATGAACACAGCCGGGAAAGACCCAGAA 424
DB 441 GACAGCGAGTCTATGCTCGGGA-CGGGATGAACACAGACCGGGGAAAGACCCAGAA 499
QY 425 GTCACCCCTGATGTCACAGTGAATACAGGCCATCATCGGAGAGACGCCAATGCCTGAG 484

500 GTCACCCCTGAATGTCACAGTGAATAGAGCCATATGGAAGAGAGAGCCAAATGCCTGAG 559
485 ACTCCAAAATGGTTTCATCTGCCCTATTTGTTCCAGATGCTCCATATGCCAGTTCTTC 544
560 ACTCCAAAATGGTTTCATCTGCCCTATTTGTTCCAGATGCTCCATATGCCAGTTCTTC 619
545 AAATTCGTAAAC--CAGAGTTACACACAGCAGC--TCAAAGGGGAGAGTCCCTCCAGTTCAC 601
620 ACATTCGTAAACCGCAGAGTTACACACAGCAGCTTCAAAGGGGAGAGTCCCTCCAGTTCAC 679
602 CACTCTCTCCCCACACACCCAAA--TCAGCCACCGCC--TCGAGTGTCCAGAGCATCTTCAG 659
680 CACTCTCTCCCCACACACCCAAAATTCACCCACCGCCCTTCGAGTGTTCAGAGCATCTTCAG 739
660 TAGCAGGTGACAAAGCCCGC--AACCTTCTCTGCCATTCACACTACAGCTCAAAAATCTCAGT 718
740 TAGCAGGTGACAAAGCCCGCAACTTCTCTGCCATTCACACTACAGCTCAAAAATCTCAGT 799
719 CTGGAGGGGCTGCTCAAGCCCC--AGACGCCAGCTTACACACACACACACAGGCTGCAC 775
800 CTGGAAGGGCTGCTTCAAGCCCCAGAGCCCGCCAGCTTACAA--CANACACACAGGCTGCAC 858
776 AGCAGAGAGCAGCTGGACTATGGCTCACAGTCTGGGAGGAGGAGGCCAAGG 825
859 AGCAGAGAGCAGCTGGACTATGGCTCACAGTCTGGGAGGAGGAGGCCAAGG 908

RESULT 4
US-09-724-864-11
; Sequence 11 Application US/09724864
; Patent No. 6380362
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Murison, James G.
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed
; TITLE OF INVENTION: by the polynucleotides and methods for their use.
; FILE REFERENCE: 11000.105001
; CURRENT APPLICATION NUMBER: US/09/724,864
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1480
; TYPE: DNA
; ORGANISM: Mouse
; US-09-724-864-11

Query Match 29.5%; Score 563.6; DB 4; Length 1480;
Best Local Similarity 67.5%; Pred. No. 5.4e-159;
Matches 940; Conservative 0; Mismatches 389; Indels 63; Gaps 8;

QY 62 CTAGAAGGGACAATGGAGCTTCTGGCTTTGGCCACTTTACTTCTGCCAGTATCAGGGGCC 121
DB 43 CTCAGGGAACCATGGAGCTTTTGGCTTTGGTTACTTTACTTCTGCCAGTCTCTGGGCC 102
QY 122 CTGAGGATCTCCCAAGAGTAAGGTAGAGGGGAGCTGGGGGATCAGTTTACCATCAA 181
DB 103 CTGAGAGCTCTCCCAAGAGTACAGTGAATGTAGAGTGGGTGGATCATTCATCGAA 162
QY 182 TGCCCACTCTGAAATGTCATGTAGGATATCTGTCCCGGAGATGGCTGGATCTGGA 241
DB 163 TGCCCACTCTCTCACTACAGTGAAGTATCTGTCTCGCAGATGGCCAACTGGG 222
QY 242 ACATGTGTACCGTGTATCCACCACCACTTCATCAAGGAGAGATACAAAGGCCAGTT 301
DB 223 ATATGCTCCACTGTGGTGTCCCAACAC---CTTTGTCAAGAGGAATATGAAGGCGAGT 279
QY 302 ACTCTGAAGCAATACCCACGCAAGAACTCTGTCTCTAGTGGAGTAAACACAGCTGACAGAA 361
DB 280 ACCCTGACGCCATGCTTGGATAAAGAGCTATTCCTTAGTGGAGATGACACAGCTGACGAA 339
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[illegible]

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RESULT 6
US-09-232-160-16
; Sequence 16, Application US/09232160
; Patent NO. 6368794
; GENERAL INFORMATION:
; APPLICANT: Steve Daniel
; APPLICANT: James Gilmore
; APPLICANT: Susan G. Stuart
; APPLICANT: Laura Stuve
; TITLE OF INVENTION: DETECTION OF ALTERED EXPRESSION OF GENES REGULATING CELL
; TITLE OF INVENTION: PROLIFERATION
; FILE REFERENCE: PA-0003 US
; CURRENT APPLICATION NUMBER: US/09/232.160
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PERL Program
; SEQ ID NO 16
; LENGTH: 2430
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 3688209
US-09-232-160-16

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	Query Match	2.5%	Score 48.2;	DB 4;	Length 2430;
	Best Local Similarity	43.3%;	Pred. No.	0.00045;	
Matches	Conservative	0;	Mismatches	293;	Indels 0; Gaps 0;
QY	544	CAAAATTCGTTAACAGAGATTACCAACCAGCAGCTCAAAGGGCGAAGTCCCTCCAGTGTCACCA	603		
Db	1162	CAAGTTCAGGTACAGCCCTGCAGGCCCTTCGAGGCTCTCTGGTGTGTGGCAC	1221		
QY	604	CTCCTCCCCCACCACCAATAACACCCACCGCCCTCGAGTGTCTCCAGAGCACTTCACGTACG	663		
Db	1222	TACCTCGAGAAGACCTCCAGACACCATCTCGGCTGTGCATATGGSCACTCGCAGCTGT	1281		
QY	664	AGGTGAACAACCCCGGAACCTTCTCGCCATCCACTACAGCTCAAAAATCTTCAGCTCTGGA	723		
Db	1282	GCTGGGCATGGCAGGAGGGTGTCTACCTACACAGCCCCCGCTGTCTCTCTCAACCA	1341		
QY	724	GGGGCTCTCAAGCCCCCAGACGCCACGCTACAACCCACACACAGGCTGCACAGGACAG	783		
Db	1342	GGGAGGGCCATGTCCCTATCAGATGCCCTGAAGGGGTTACTGACAACTGTGTGGACAC	1401		
QY	784	AGCACTGGACTATGGCTTCACAGTCTGGAGGGAGGCCAAGGATTTTCACATCTCTGATCCC	843		
Db	1402	AGTGGTGATTAACGTGGCGCTTCCCGAGCTGTCCGCTGATGAGCCCGAGACGAAATTCG	1461		
QY	844	GACCATCTGGCGCTTTTCCCTGTCTGGCACTTCTGGGGCTGGTGTGAAAAAGGGCCGTGA	903		
Db	1462	GGACATGCACAACCCACAGCCGAGGTCTGAGCGCGGAGGCGGAGCGCAGAGCGTCTGG	1521		
QY	904	AAGGAGGAAGCCCTCTCCAGCGGGCGCGCCGACTGCGCGTAGGATGCGCGCCCTGGA	963		
Db	1522	GGCGCGTTCGCGCGGCGCGAGCCCGCCCGCGTCTGCGACAGCCCGCCGACGCGCTCG	1581		
QY	964	GAGTCCCGAGAGGCCCGCGGGTTCGCGCGACCGCGCTCCCCAAACAAATCTACAGCGC	1023		
Db	1582	CAGCGCGCAGAGCCCGCGCGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	1641		

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QY      1024  CTGCGCCGCGCGCCCTGCTGAGCGGAGCGCTGCAGGC 106
Db      1642  CGCAGCGCCGCGCGCGCTTCGCGCGCTGCCCGC 1678

RESULT 7
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFELINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fls
; US-08-232-463-14

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	Query Match	2.3%, Score 43.4; DB 1; Length 7218;
	Best Local Similarity	3.0%; Pred. No. 0.024; Indels 0; Gaps 0;
	Matches 11; Conservative 207; Mismatches 153;	
QY	136 AGAAGTAAAGTCACAGGGGAGCTGGCGGATCAGTTACCATCAATATGCCCATCTTGTA	195
DB	1415 RR	1356
QY	196 AATGCATGTGAGGATATATCTGTCGCCGGAGATGGCTGGATCTGGAAACATGTGGTACCGT	255
DB	1355 RR	1296
QY	256 GGATCCACCAACACTCATCAAGGCAGGAATACAAGGCCGAGTTACTCTGAACCAATA	315
DB	1295 RR	1236
QY	316 CCCACGGCAAGATCTGTTCTTAGTGGAGGTAAACACAGCTACAGAAAGTACACGCGGAGT	375



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;
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; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1433 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   FEATURE:
;     NAME/KEY: Coding Sequence
;     LOCATION: 118...1101
;   OTHER INFORMATION:
;     NAME/KEY: Coding Sequence
;     LOCATION: 118...234
;   OTHER INFORMATION:
;     NAME/KEY: Coding Sequence
;     LOCATION: 235...1101
;   OTHER INFORMATION:
;     PUBLICATION INFORMATION:
;       AUTHORS: Binkert, C., et al.
;       TITLE: Cloning, sequence analysis and expression....
;       JOURNAL: EMBO J.
;       VOLUME: 8
;       ISSUE: 1989
;       PAGES: 2497-2502
;       DATE:
;
; US-09-199-926-1
;
; Query Match      2.2%; Score 41.8; DB 3; Length 1433;
; Best Local Similarity 46.7%; Pred. No. 0.027;
; Matches 133; Conservative 0; Mismatches 152; Indels 0; Gaps 0;
;
; QY 841 CCGAGCATCTCTGGGCTTTCTGCTGGCACTTCTGGGCTGGTGGTGAAGAGGCCGT 900
;   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; Db 366 CCGAGCAGCTCGCGCATGCGATGGGGGCGCTCGGGCCACTGCGGGCCACCCCGGGG 307
;
; QY 901 TGAAGAGGAAGACCTCTCCAGGCGGGCGCCCGCGACTGGCGTGAGGATGCGGCCCT 960
;   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; Db 306 CGGCGCAACGGCGGGGCGCGCAGCGGCCAGGCGCTCGGGTGTGCGAGGGCGGACG 247
;
; QY 961 GGAGAGCTCCAGAGCGCCCGGGTCTGGCGGCGGCGGCTCCCAAAACACATCTACG 1020
;   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; Db 246 GAACAGCACTTCGCGCGGCGCCCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCG 187
;
; QY 1021 CGCCTCCCGCGGCGGCTGTGGAGCGACGCTGCAGGCACAGGGGAGGCGCCCGCTTC 1080
;   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; Db 186 CAGCGCAGCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 127
;
; QY 1081 CGGCCCCGAGCGCCCTTGGCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1125
;   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; Db 126 CGGCGCATGCTGGCGTGGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 82
;
; RESULT 10
; US-09-128-155-16
; Sequence 16, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; EARLIER FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 152331
; TYPE: DNA
;
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(152331)
; OTHER INFORMATION: n = A,T,C or G
; US-09-128-155-16
;
; Query Match      2.1%; Score 40.8; DB 3; Length 152331;
; Best Local Similarity 47.8%; Pred. No. 0.88;
; Matches 117; Conservative 0; Mismatches 128; Indels 0; Gaps 0;
;
; QY 915 CCCTCTCCAGGCGGCGCGGCTGCGGCTGAGGATGCGGCGCTGAGAGGCTCCGAGA 974
;   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; Db 21916 CCGNGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 21975
;
; QY 975 GCGCCCGCGGCTGCGGCGGCGGCTCCCAAAACACATCTACAGGCTGCGCGGCG 1034
;   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; Db 21976 CCGCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 22035
;
; QY 1035 GCGCTGCTGGAGCGGAGCGGTGCGAGGCACAGGGAGGCGCCCGTTCCGCGCGCGGAGCGC 1094
;   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; Db 22036 CCGCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 22095
;
; QY 1095 CGTTGCGCGCGGCGGCGGCTGCGAGGTGCTGAATCTGCTGCTGCTGCTGCTGCTG 1154
;   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; Db 22096 CCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 22155
;
; QY 1155 AGACC 1159
;   ||
; Db 22156 CCGCC 22160
;
; RESULT 11
; US-09-368-590-1/c
; Sequence 1, Application US/09368590
; Patent No. 6187563
; GENERAL INFORMATION:
; APPLICANT: Solimena, Michele
; TITLE OF INVENTION: INTERACTING POLYPEPTIDES FOR
; FILE REFERENCE: 101918-200 (OCR-941)
; CURRENT APPLICATION NUMBER: US/09/368,590
; EARLIER FILING DATE: 1999-08-04
; EARLIER APPLICATION NUMBER: 60/095,657
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 7812
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(6879)
; NAME/KEY: unsure
; LOCATION: (100)...(102)
; NAME/KEY: unsure
; LOCATION: (1021)...(1023)
; NAME/KEY: unsure
; LOCATION: (2266)...(2268)
; US-09-368-590-1
;
; Query Match      2.1%; Score 40.6; DB 3; Length 7812;
; Best Local Similarity 50.5%; Pred. No. 0.17;
; Matches 97; Conservative 0; Mismatches 95; Indels 0; Gaps 0;
;
; QY 924 GCGGGCGCGCGGCGGCTGCGGCTGAGGATGCGGCGGCTGAGAGCTCCGAGAGCGCGCGG 983
;   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; Db 1164 GTCATGCGCGCGCGCGCGCTGTTCCCGCTGCGCGCGCTGCGCGCGCGCGCGCGCGCG 1105
;
; QY 984 GGTGCGCGCGGCGGCGGCTCCCAAAACACATCTACAGGCTGCGCGGCGGCGGCGCTG 1043
;   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; Db 1104 CGCAGCTCCAGGAGAGGCTCTTGTGTGCGGCGGCGGCGGCTCTGCGGCTCTCCAGCT 1045
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Qy	1044	GACGGAGCGTGACGAGCACAAGGAGGCCCCCTTC	CCGGCCCCCGAGCGCGCTGC	CCCC	1103
Dδ	1044	CACGAGGGCCACAGCGTCCGNGAAGCCTCACGT	CCGGCGTCCGCGCGCTGC	TGCTC	985
Qy	1104	CCGCCCCGCTGC	1115		
Dδ	984	CTCAGCTCGC	973		

RESULT 12

US-09-252-991A-1441/c

; Sequence 1441, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 1441

; LENGTH: 636

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-1441

Query Match	2.1%	Score 39.2;	DB 4;	Length 636;
Best Local Similarity	48.6%	Pred. No. 0.1;		
Matches 107; Conservative	0;	Mismatches 113;	Indels	Gaps 0;
QY	876	TGGGGCTGGTGGTGAAGAAGGCGCGTTGAAGGAGGAAGCCCTCTCCAGGGGGCCGCC	935	
Db	584	TGCGGCGGAGAGCCGATCGAGGGCCGAGCTGGGGAACATGCCGAACAGCGCGCT	525	
QY	936	GATTGCGCGTGGAGATCGGCGCCTTGAGAGCTCCAGAGCGCCCGGGTTCGCGGGAC	995	
Db	524	TGCGCGGCGCGCGGTTCCTCGTGCCAGCAGCGCGCGCCCTACTCGCGCGCGAGGC	465	
QY	996	CGCGCTCCCAAAACAACATCTACAGCGCCTCGCGCGCGCGCTCTGTGGAGCGACGCTG	1055	
Db	464	CGAGGCGCTTGCGGAAGCGCAGCACCGAGCAAGCAACGGCGCCCATAGCCCATGCTG	405	
QY	1056	CAGGCACAGGGAGGCCCCCTTCCCGGCCCGGAGCGCC	1095	
Db	404	TCGTAACCGGGGAGGACGGGATCAGGTTGGTGACACCC	365	

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RESULT 13
US-09-252-991A-1675
; Sequence 1675, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1675
; LENGTH: 1131
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa

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US-09-252-991A-1675

	Query Match.	2.1%;	Score 39.2;	DB 4;	Length 1131;
	Best Local Similarity	48.6%;	Pred. No. 0.14;		
	Matches 107;	Conservative 0;	Mismatches 113;	Indels 0;	Gaps 0;
Qy	876	TGGGCTGTGGTCAAAAGGSCCCTTGAAAGAGAGAAAGCCCTTCACAGCGGGGCCGCC	935		
Db	801	TGCGGGGAGGAAGCCGATCGACGGCGCGAGCTGGGGAACAATCCGGAACACGAGCGCGCT	860		
Qy	936	GACTTGGCCGTGAGATGGGCGCCCTGTGAGAGCTCCCAGAGCGCCCCGGGGTTGC CGCGGAC	995		
Db	861	TGCGCGCGCGCGCTTCTCGTGTGCCAAGCACGCGGGCGCGCCGCCACTTGC GCGCCGAGGC	920		
Qy	996	CGCGCTCCCAAAAACAACATCTACAGCGCCTGCCCGCGCGCGCTGTGTGAGCGGACCGCT	1055		
Db	921	CGAGGCGCTTGGCCGAAACCGCAGACGAGAGCAGCAACGCGGCCCATAGCCGATCTGT	980		
Qy	1056	CAGGACAGGGGAGGCCGCCCTTCCCGGCCCGCGAGCGCC	1095		
Db	981	TCGTAAACGGGGAGGAGCGCGGATCAGGGTGGTGGACACC	1020		

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RESULT 14
US-09-252-991A-1539/c
; Sequence 1539, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1539
; LENGTH: 1671
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1539

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	Query Match	2.1%	Score 39.2;	DB 4;	Length 1671;
	Best Local Similarity	48.6%;	Pred. No. 0.18;		
	Matches 107;	Conservative 0;	Mismatches 113;	Indels 0;	Gaps 0;
QY	876	TGGGGCTGGTGTGTAAGAGGGCCGTTCAAAGGAGGAAAGCCCTCTCCAGGGCGGCCGCC	935		
Db	1551	TGGCGGCGAGAACCGCATGACGGGCGGAGCTGGGGAACAATCCCAACGAGCGGCGCT	1492		
QY	936	GACTGGCGGTAGGATCGGCGCCCTGGAGAGTCTCCAGAGGCCCGCGGGTCCGCGGAC	995		
Db	1491	TGCGCGCGCGCGCTTCTCGGTGCCAGCAGCGCGGCGCGCCCACTCGCGCGGAGGC	1432		
QY	996	CGGCTCCCAAAACAACATCTACAGCGCTTCCCGCGCGCGCGTCTGTGGAGCGGACGCTG	1055		
Db	1431	CGAGGCGCTTGGCGGAAGCGCAGCACCGCAGAGCAGCAACGCGCCCACTAGCCGATCGT	1372		
QY	1056	CAGCACAGGGGAGGCCCGCTTCCGCGCCCGGAGGCC	1095		
Db	1371	TCGTAAACCGGGAGAGCCCGATCAGGTTGTTGCACACC	1332		

RESULT 15  
US-03-160-496-4  
; Sequence 4, Application US/09160496  
; Patent No. 6346613  
; GENERAL INFORMATION:  
; APPLICANT: O'Mahony, Daniel J  
; APPLICANT: Cagney, Gerard

```

; TITLE OF INVENTION: Composition and Method for Enhancing Paracellular
; TITLE OF INVENTION: Transport across Cell Layers
; FILE REFERENCE: Docket No. 6346613; 98.1070.US
; CURRENT APPLICATION NUMBER: US/09/160,496
; CURRENT FILING DATE: 1998-09-24
; EARLIER APPLICATION NUMBER: US 60/059,644
; EARLIER FILING DATE: 1997-09-24
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1920
; TYPE: DNA
; ORGANISM: Gallus gallus
; PUBLICATION INFORMATION:
; TITLE: Occludin: A novel integral membrane protein localizing
; TITLE: at tight junctions
; JOURNAL: J. Cell Biol.
; VOLUME: 123
; ISSUE: 6
; PAGES: 1777-1788
; DATE: Dec 1993
; DATABASE ACCESSION NUMBER: D21837
US-09-160-496-4

Query Match          2.0%; Score 38.4; DB 4; Length 1920;
Best Local Similarity 47.5%; Pred. No. 0.34;
Matches 114; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

QY 748 CAGCTACACACCACAGGCTGCACAGGAGAGGACCTGGACTATGGCTCACAGTC 807
Db 314 CGGCTCCAACTACTACGCGAGGGGCTGAGCTACAGCTACGGGCTAGGGGGCTACTACGG 373
QY 808 TGGGAGGAAGGCCAAGGATTTCATCTGATCCCGACCACTCTTGGGCTTTTCTGCT 867
Db 374 AGGGGTGAACCAAGCCAGCGCCACGGCTTCATGATCGCATGGCGTCTGCTTCTCT 433
QY 868 GGCACCTTCTGGGCTGGTGGTGAAGAGGCGCTTGAAGAGGAGGAAGCCCTCTCAGGGC 927
Db 434 GCGCCAGCTGGGGCTGCTGGTGGCGGCTCAGCAATCCGGGGCCACGCGCTCGCGGG 493
QY 928 GCGCGCGGACTGGCGCTGAGGATGCGGCGCTGGAGAGCTCCAGAGGCGCGCGGGTC 987
Db 494 CTTCTACCTGGCGCTGCTGGTGTGAGCGCGCTGCTGGCCCTTCGTCATGCTCATGCCCTC 553

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Search completed: September 14, 2003, 02:14:02  
Job time : 129 secs